GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 13:20:30 ; Search time 88.4866 Seconds
(without alignments)
869.796 Million cell updates/sec

Title: US-09-816-653A-2
Perfect score: 1061
Sequence: 1 MSQPAGNQTSPGATEDYSYG.....WAHLGVQVWQRAECPQVPKI 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1059	99.8	199	6	ABB99462	Abb99462 Amino aci
2	1048	98.8	487	5	AAO17374	Aao17374 Human ret
3	1048	98.8	666	6	ABU82087	Abu82087 Novel hum
4	1048	98.8	667	4	AAU04557	Aau04557 Human Str
5	1048	98.8	667	4	AAB88572	Aab88572 Human hyd
6	1048	98.8	667	5	AAU83631	Aau83631 Human PRO
7	1048	98.8	667	5	AAU78575	Aau78575 Human Str
8	1048	98.8	667	5	AAO19413	Aao19413 Human mol
9	1048	98.8	667	6	ADA54816	Ada54816 Human pro
10	1048	98.8	667	6	ABU80778	Abu80778 Human PRO
11	1048	98.8	667	6	ABO33744	Abo33744 Novel hum
12	1048	98.8	667	6	ABJ72267	Abj72267 Human PRO
13	1048	98.8	667	6	ABJ72395	Abj72395 Human PRO
14	1048	98.8	667	6	ABO34290	Abo34290 Human sec
15	1048	98.8	667	7	ABJ72097	Abj72097 Human mem
16	1048	98.8	667	7	ADB83570	Adb83570 Novel hum
17	1048	98.8	667	7	ADB80676	Adb80676 Novel hum
18	1048	98.8	667	7	ADB73217	Adb73217 Novel hum
19	1048	98.8	667	7	ADB78299	Adb78299 Novel hum
20	1048	98.8	667	7	ADB84947	Adb84947 Human PRO
21	1048	98.8	667	7	ADB78053	Adb78053 Novel hum
22	1048	98.8	667	7	ADB87119	Adb87119 Human PRO
23	1048	98.8	667	7	ADB84701	Adb84701 Human PRO
24	1048	98.8	667	7	ADB83816	Adb83816 Novel hum
25	1048	98.8	667	7	ADB72971	Adb72971 Novel hum
26	1048	98.8	667	7	ADC36809	Adc36809 Human PRO
27	1048	98.8	667	7	ADC21799	Adc21799 Human PRO
28	1048	98.8	667	7	ADC49830	Adc49830 Novel hum
29	1048	98.8	667	7	ADC49029	Adc49029 Novel hum
30	1048	98.8	667	7	ADC49546	Adc49546 Novel hum
31	1048	98.8	667	7	ADC47407	Adc47407 Novel hum
32	1048	98.8	667	7	ADC47152	Adc47152 Novel hum
33	1048	98.8	667	7	ADC78027	Adc78027 Novel hum
34	1048	98.8	667	7	ADD06262	Add06262 Novel hum
35	1048	98.8	667	7	ADC77781	Adc77781 Novel hum
36	1048	98.8	667	7	ADD50744	Add50744 Novel hum
37	1048	98.8	667	7	ADD50990	Add50990 Novel hum
38	1048	98.8	667	7	ADD50471	Add50471 Human PRO
39	1048	98.8	667	7	ADD50225	Add50225 Human PRO
40	1048	98.8	667	7	ADD51236	Add51236 Novel hum
41	1048	98.8	667	8	ADC48783	Adc48783 Novel hum
42	1048	98.8	667	8	ADE20954	Ade20954 Novel hum
43	1048	98.8	667	8	ADE05798	Ade05798 Human PRO
44	1048	98.8	667	8	ADD75027	Add75027 Human PRO
45	1048	98.8	667	8	ADD75773	Add75773 Novel hum

ALIGNMENTS

RESULT 1
ABB99462
ID ABB99462 standard; protein; 199 AA.
XX
AC ABB99462;
XX
DT 12-FEB-2003 (first entry)
XX
DE Amino acid sequence of the amino-terminal of human STRA6.
XX
KW Human; STRA6; retinoic acid; hSTRA6; Wnt-1; cellular transformation;
KW tumour; colon cancer; breast cancer; melanoma; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 31
FT /note= "unknown residue encoded by GNN"
XX
PN WO200277027-A1.
XX
PD 03-OCT-2002.
XX
PF 23-MAR-2001; 2001WO-US009561.
XX
PR 23-MAR-2000; 2000US-0191532P.
XX
PA (CURA-) CURAGEN CORP.
PA (GETH) GENENTECH INC.
XX
PI Rastelli LK, Pennica D;
XX
DR WPI; 2003-058366/05.
DR N-PSDB; ABV76852.
XX
PT New human STRA6 (stimulated by retinoic acid) proteins and nucleic acids
PT encoding the proteins, useful for treating cancers (e.g. colon and breast
PT cancer, or melanoma), or in gene therapy.
XX
PS Claim 4; Page 9-10; 113pp; English.
XX
CC The present sequence represents the amino-terminal portion of a human
CC protein, designated STRA6 (stimulated by retinoic acid). hSTRA6 (human
CC STRA6) is modulated by Wnt-1 and plays a role in cellular transformation.
CC The hSTRA6 nucleic acids and proteins are useful for treating tumours
CC (e.g. colon and breast cancer, or melanoma), in gene therapy, in
CC diagnostic applications where the presence or amount of the nucleic acid
CC or protein is to be assessed, and in the generation of antibodies that

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CC   bind immunospecifically to these sequences for therapeutic and diagnostic
CC   applications. hSTRA6 nucleic acid fragments may be used as hybridization
CC   probes to identify hSTRA6-encoding nucleic acids, or as PCR primers for
CC   amplification and/or mutation of hSTRA6 molecules
XX
SQ   Sequence 199 AA;

  Query Match             99.8%;  Score 1059;  DB 6;  Length 199;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-107;
  Matches  199;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 MSQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSI 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MSQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSI 60

Qy         61 LVLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDE 120

Qy        121 DALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSW 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSW 180

Qy        181 AHLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||||
Db        181 AHLGVQVWQRAECPQVPKI 199


RESULT 2
AAO17374
ID   AAO17374 standard; protein; 487 AA.
XX
AC   AAO17374;
XX
DT   08-JUL-2002  (first entry)
XX
DE   Human retinoic acid responsive protein 53-57.
XX
KW   Human; retinoic acid responsive protein 53.57; arrhythmia;
KW   bronchial asthma; peptic ulcer; diabetes; cancer; cytostatic; antiulcer;
KW   antiasthmatic; antidiabetic; endocrine; cardiant;
KW   embryonic development disorder; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO200226808-A1.
XX
PD   04-APR-2002.
XX
PF   20-AUG-2001; 2001WO-CN001252.
XX
PR   23-AUG-2000; 2000CN-00119715.
XX
PA   (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX
PI   Mao Y,  Xie Y;
XX
DR   WPI; 2002-330093/36.
DR   N-PSDB; AAL45968.
XX
PT   Human retinoic acid responsive protein 53.57 and encoding polynucleotide,
PT   used in diagnosis and treatment of diseases e.g., arrhythmia, asthma,
PT   diabetes and cancer.
XX
PS   Claim 1; Page 32-33; 37pp; Chinese.
XX
CC   The present invention provides the protein and coding sequences of human
CC   retinoic acid responsive protein 53.57. The sequences can be used in the
CC   treatment of arrhythmia, bronchial asthma, peptic ulcer, diabetes, cancer
CC   and embryonic development disorders. The present sequence is the protein
CC   of the invention
XX
SQ   Sequence 487 AA;

  Query Match             98.8%;  Score 1048;  DB 5;  Length 487;
  Best Local Similarity   99.0%;  Pred. No. 8.8e-106;
  Matches  196;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200


RESULT 3
ABU82087
ID   ABU82087 standard; protein; 666 AA.
XX
AC   ABU82087;
XX
DT   26-JUN-2003  (first entry)
XX
DE   Novel human secreted and transmembrane protein PRO10282.
XX
KW   Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
KW   antiangiogenic; hypotensive; vulnenry; antiarteriosclerotic;
KW   gene therapy; cardiovascular disorder; endothelial disorder;
KW   angiogenic disorder; cardiac hypertrophy; trauma; cancer;
KW   age-related macular degeneration; atherosclerosis; hypertension;
KW   arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
KW   thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
KW   liver carcinoma; wound healing; chromosome mapping; gene mapping.
XX
OS   Homo sapiens.
XX
PN   US2003088063-A1.
XX
PD   08-MAY-2003.
XX
PF   12-AUG-2002; 2002US-00219003.
XX
PR   25-JUL-2000; 2000US-0220664P.
PR   01-JUN-2001; 2001WO-US017800.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-APR-2002; 2002US-00119480.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Desnoyers L,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Smith V,  Stephan JF,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-393229/37.
XX
PT   One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT   useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT   infarction), endothelial or angiogenic disorders in a mammal.
XX
PS   Claim 11; Fig 80; 314pp; English.
XX
CC   The invention describes one hundred and eighty seven nucleic acids
CC   encoding novel human secreted and transmembrane (PRO) polypeptides. The
CC   PRO nucleic acids, polypeptides, agonists and antagonists are useful for
CC   treating or diagnosing a cardiovascular, endothelial or angiogenic
CC   disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
CC   related macular degeneration, atherosclerosis, hypertension, arterial
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CC   restenosis, rheumatoid arthritis, angina, myocardial infarctions,
CC   thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
CC   carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
CC   have applications in molecular biology, including use as hybridisation
CC   probes, and in chromosome and gene mapping. This is the amino acid
CC   sequence of a novel human secreted and transmembrane PRO polypeptide
XX
SQ   Sequence 666 AA;

  Query Match             98.8%;  Score 1048;  DB 6;  Length 666;
  Best Local Similarity   99.0%;  Pred. No. 1.3e-105;
  Matches  196;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
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Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
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Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200


RESULT 4
AAU04557
ID   AAU04557 standard; protein; 667 AA.
XX
AC   AAU04557;
XX
DT   26-SEP-2001  (first entry)
XX
DE   Human Stra6 homologue, PRO10282.
XX
KW   Human; Stra6; PRO10282; 15q23; tumour; breast cancer; head tumour;
KW   leukaemia; lymphoid malignancy; inflammatory disorder;
KW   immunogenic disorder; antigen; antibody.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   8. .12
FT                   /note= "Asn is N-glycosylated"
FT   Region          50. .56
FT                   /label= N_myristoylation_site
FT   Domain          54. .69
FT                   /label= Transmembrane_domain
FT   Region          89. .97
FT                   /note= "Region deleted in Stra6 variant PRO19578"
FT   Domain          102. .119
FT                   /label= Transmembrane_domain
FT   Region          132. .140
FT                   /note= "ATP/GTP-binding site motif A (P-loop)"
FT   Domain          148. .166
FT                   /label= Transmembrane_domain
FT   Region          176. .182
FT                   /label= N_myristoylation_site
FT   Domain          207. .222
FT                   /label= Transmembrane_domain
FT   Region          241. .247
FT                   /label= N_myristoylation_site
FT   Domain          301. .320
FT                   /label= Transmembrane_domain
FT   Region          317. .323
FT                   /label= N_myristoylation_site
FT   Region          341. .347
FT                   /label= N_myristoylation_site
FT   Domain          364. .380
FT                   /label= Transmembrane_domain
FT   Region          364. .375
FT                   /note= "Prokaryotic membrane lipoprotein attachment site"
FT   Domain          431. .451
FT                   /label= Transmembrane_domain
FT   Domain          474. .489
FT                   /label= Transmembrane_domain
FT   Region          525. .531
FT                   /label= N_myristoylation_site
FT   Domain          560. .535
FT                   /label= Transmembrane_domain
FT   Region          627. .633
FT                   /label= N_myristoylation_site
FT   Region          631. .637
FT                   /label= N_myristoylation_site
FT   Region          640. .646
FT                   /label= N_myristoylation_site
FT   Region          661. .667
FT                   /label= N_myristoylation_site
XX
PN   WO200151635-A2.
XX
PD   19-JUL-2001.
XX
PF   11-JAN-2001; 2001WO-US000847.
XX
PR   13-JAN-2000; 2000US-0175849P.
PR   14-APR-2000; 2000US-0197089P.
PR   29-AUG-2000; 2000US-0228914P.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Pennica D,  Smith V,  Wood WI;
XX
DR   WPI; 2001-442146/47.
DR   N-PSDB; AAS08630.
XX
PT   Human nucleic acid encoding a PRO10282 or PRO19578 polypeptide (the PRO
PT   polypeptides are referred to as Stra6 polypeptides), useful in molecular
PT   biology, including use as hybridization probes, and in chromosome and
PT   gene mapping.
XX
PS   Claim 24; Fig 2; 159pp; English.
XX
CC   The sequence is human PRO10282, a homologue of murine Stra6, a retinoic
CC   acid responsive protein thought to play an important role in early
CC   dorsoventral limb patterning during development and later in the control
CC   of endochondral ossification. The gene for the Stra6 homologue is located
CC   on chromosome 15q23. The Stra6 polypeptides, agonists, antagonists or
CC   anti-Stra6 antibodies are useful for preparation of a medicament useful
CC   in the treatment of a condition which is responsive to the Stra6
CC   polypeptides, agonists, antagonists or anti-Stra6 antibodies. The Stra6
CC   polypeptides may also be employed as molecular weight markers for protein
CC   electrophoresis. The Stra6 nucleic acids have applications in molecular
CC   biology, including use as hybridisation probes, and in chromosome and
CC   gene mapping. The antibodies and other anti-tumour compounds may be used
CC   to treat various conditions, including those characterised by
CC   overexpression and/or activation of amplified genes. Exemplary conditions
CC   or disorders include benign or malignant tumours (e.g., renal, liver,
CC   kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
CC   pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas,
CC   glioblastomas, and various head and neck tumours, leukaemias and lymphoid
CC   malignancies), neuronal, glial, astrocytal, hypothalamic and other
CC   glandular, macrophagal, epithelial, stromal and blastocoelic disorders,
CC   inflammatory, angiogenic and immunogenic disorders
XX
SQ   Sequence 667 AA;

  Query Match             98.8%;  Score 1048;  DB 4;  Length 667;
  Best Local Similarity   99.0%;  Pred. No. 1.3e-105;
  Matches  196;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;
```

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Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
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Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200
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RESULT 5
AAB88572
ID   AAB88572 standard; protein; 667 AA.
XX
AC   AAB88572;
XX
DT   04-JUN-2001  (first entry)
XX
DE   Human hydrophobic domain containing protein clone HP10713 #36.
XX
KW   Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;
KW   antianaemic; vulnerary; antiulcer; osteopathic; anti-inflammatory;
KW   cytostatic; gene therapy; autoimmune disorder; multiple sclerosis;
KW   HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing;
KW   inflammatory bowel disease; nutritional supplement; appetite; vaccine;
KW   behavioural characteristic; immune response.
XX
OS   Homo sapiens.
XX
PN   WO200112660-A2.
XX
PD   22-FEB-2001.
XX
PF   10-AUG-2000; 2000WO-JP005356.
XX
PR   17-AUG-1999;   99JP-00230344.
PR   07-SEP-1999;   99JP-00252551.
PR   01-OCT-1999;   99JP-00281132.
PR   22-OCT-1999;   99JP-00301624.
PR   04-NOV-1999;   99JP-00313877.
XX
PA   (SAGA ) SAGAMI CHEM RES CENT.
PA   (PROT-) PROTEGENE INC.
XX
PI   Kato S,  Kimura T;
XX
DR   WPI; 2001-160059/16.
DR   N-PSDB; AAF94442.
XX
PT   Human proteins with hydrophobic domains and the DNAs which encode them
PT   are useful for treating autoimmune disorders, burns and tumors and for
PT   screening novel pharmaceuticals.
XX
PS   Claim 1; Page 288-291; 518pp; English.
XX
CC   AAF94417 to AAF94516 encode the human proteins given in AAB88557 to
CC   AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant,
CC   anti-HIV, neuroprotective, antianaemic, vulnerary, antiulcer,
CC   osteopathic, anti-inflammatory and cytostatic activities, and can be used
CC   in gene therapy. (I) can be used as pharmaceuticals and as antigens to
CC   prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes
CC   for genetic diagnosis and gene sources for gene therapy or for producing
CC   (I) in large quantities. Cells containing (II) are used for the detection
CC   of ligands or receptors corresponding to membrane or secretory proteins
CC   and to screen small molecule novel pharmaceuticals. Antibodies directed
CC   to (I) can be used for the detection, quantification and purification of
CC   (I). Activities of (I) may include cytokine and cell
CC   proliferation/differentiation function, immune stimulating or suppressing
CC   activity, haematopoiesis regulating activity, tissue growth activity,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, receptor/ligand activity and anti-inflammatory
CC   activity. (I) and (II) can be used to treat autoimmune disorders e.g.
CC   multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis,
CC   inflammatory bowel disease and tumours. (I) and (II) can also be used for
CC   wound healing, as nutritional sources or supplements e.g. as amino acid,
CC   carbon or nitrogen source, to effect metabolism, catabolism, anabolism,
CC   processing and utilisation of dietary fat, protein, carbohydrate,
CC   vitamins and minerals, to effect behavioural characteristics, to affect
CC   appetite, and can act as antigens in vaccines to raise an immune response
CC   to the protein or another material cross-reactive with the protein
XX
SQ   Sequence 667 AA;

  Query Match             98.8%;  Score 1048;  DB 4;  Length 667;
  Best Local Similarity   99.0%;  Pred. No. 1.3e-105;
  Matches  196;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
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Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
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Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200
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RESULT 6
AAU83631
ID   AAU83631 standard; protein; 667 AA.
XX
AC   AAU83631;
XX
DT   08-MAY-2002  (first entry)
XX
DE   Human PRO protein, Seq ID No 80.
XX
KW   Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW   breast cancer; prostate tumour; rectal tumour; liver tumour;
KW   pericyte cell proliferation; chondrocyte cell proliferation;
KW   tumour necrosis factor-alpha.
XX
OS   Homo sapiens.
XX
PN   WO200208288-A2.
XX
PD   31-JAN-2002.
XX
PF   29-JUN-2001; 2001WO-US021066.
XX
PR   20-JUL-2000; 2000US-0219556P.
PR   25-JUL-2000; 2000US-0220585P.
PR   25-JUL-2000; 2000US-0220605P.
PR   25-JUL-2000; 2000US-0220607P.
PR   25-JUL-2000; 2000US-0220624P.
PR   25-JUL-2000; 2000US-0220638P.
PR   25-JUL-2000; 2000US-0220664P.
PR   25-JUL-2000; 2000US-0220666P.
PR   26-JUL-2000; 2000US-0220893P.
PR   28-JUL-2000; 2000WO-US020710.
PR   01-AUG-2000; 2000US-0222425P.
PR   22-AUG-2000; 2000US-0227133P.
```

PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2002-172001/22.
DR N-PSDB; ABK33575.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumors such
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
PT or liver tumor.
XX
PS Claim 11; Fig 80; 359pp; English.
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention
XX
SQ Sequence 667 AA;

Query Match 98.8%; Score 1048; DB 5; Length 667;
Best Local Similarity 99.0%; Pred. No. 1.3e-105;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              ||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200
```

RESULT 7
AAU78575
ID AAU78575 standard; protein; 667 AA.
XX
AC AAU78575;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human Stra6 (PRO10282) protein.
XX
KW Human; cancer; Stra6; PRO10282; cytostatic; stromal disorder; tumour;
KW retinoid; Wnt; tumour antigen; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytal disorder;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; blastocoelic disorder; chromosome 15q23.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Region	8. .12
FT		/note= "N Glycosylation site"
FT	Region	50. .56
FT		/note= "N-myristoylation site"
FT	Domain	54. .69
FT		/note= "Transmembrane domain"
FT	Domain	102. .119
FT		/note= "Transmembrane domain"
FT	Region	132. .140
FT		/note= "ATP/GTP binding site motif A"
FT	Domain	148. .166
FT		/note= "Transmembrane domain"
FT	Region	176. .182
FT		/note= "N-myristoylation site"
FT	Domain	207. .222
FT		/note= "Transmembrane domain"
FT	Region	241. .247
FT		/note= "N-myristoylation site"
FT	Domain	301. .320
FT		/note= "Transmembrane domain"
FT	Region	317. .323
FT		/note= "N-myristoylation site"
FT	Region	341. .347
FT		/note= "N-myristoylation site"
FT	Domain	364. .380
FT		/note= "Transmembrane domain"
FT	Region	364. .375
FT		/note= "lipoprotein lipid attachment site"
FT	Domain	431. .451
FT		/note= "Transmembrane domain"
FT	Domain	474. .489
FT		/note= "Transmembrane domain"
FT	Region	525. .531
FT		/note= "N-myristoylation site"
FT	Domain	560. .535
FT		/note= "Transmembrane domain"
FT	Region	627. .633
FT		/note= "N-myristoylation site"
FT	Region	631. .637
FT		/note= "N-myristoylation site"
FT	Region	640. .646
FT		/note= "N-myristoylation site"
FT	Region	661. .667
FT		/note= "N-myristoylation site"

XX
PN WO200218608-A2.
XX
PD 07-MAR-2002.
XX
PF 10-JUL-2001; 2001WO-US021635.
XX
PR 29-AUG-2000; 2000US-0228914P.
PR 11-JAN-2001; 2001US-00759056.
PR 10-JUL-2001; 2001US-00901812.
XX
PA (GETH) GENENTECH INC.
XX
PI Tice D, Pennica D, Polakis P, Szeto W;

XX
DR WPI; 2002-292202/33.
DR N-PSDB; ABK47278.
XX
PT Selectively enhancing the expression of a protein in a tumor cell
PT characterized by aberrant Wnt signaling, useful for enhancing the
PT efficacy of treatment of cancers, comprises treating the tumor cell with
PT a retinoid.
XX
PS Example 1; Fig 2; 141pp; English.
XX
CC This invention relates to a novel method for selective enhancement of the
CC expression of a protein in a tumour cell characterised by aberrant Wnt
CC signalling by treating the tumour cell with a retinoid. The method is
CC useful for enhancing the efficacy of treatment of cancers characterised
CC by aberrant Wnt signalling, and for identifying tumour antigens the
CC expression of which is selectively enhanced by retinoid treatment. The
CC method is also useful in the early detection of tumours for early
CC intervention. The tumour antigens are useful as targets for cancer
CC therapy, since selective enhancement of their expression by retinoid
CC treatment relative to normal cells improves the efficacy and therapeutic
CC index of cancer therapeutics directed against these antigens. Antibodies
CC binding to the tumour antigens may be administered for the treatment of
CC various disorders or conditions, including those characterised by
CC overexpression and/or activation of the tumour antigens, where such
CC conditions or disorders include benign or malignant tumours; leukaemias
CC and lymphoid malignancies; neuronal, glial, astrocytal, hypothalamic and
CC other glandular, macrophagal, epithelial, stromal and blastocoelic
CC disorders. The present sequence represents the human Stra6 protein
CC (PRO10282) which is selectively upregulated by retinoid using the method
CC of the invention. The gene encoding the human Stra6 protein is located on
CC human chromosome 15q23
XX
SQ Sequence 667 AA;

Query Match 98.8%; Score 1048; DB 5; Length 667;
Best Local Similarity 99.0%; Pred. No. 1.3e-105;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200
```

RESULT 8
AAO19413
ID AAO19413 standard; protein; 667 AA.
XX
AC AAO19413;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human molecule for disease detection and treatment protein #16.
XX
KW Human; molecule for disease detection and treatment; MDDT; gene therapy;
KW cytostatic; antiarteriosclerotic; hepatotropic; anti-HIV; antiallergic;
KW antiinflammatory; antiasthmatic; cerebroprotective; nootropic;
KW neuroprotective; antiparkinsonian; cardiant; antianginal.
XX
OS Homo sapiens.
XX
PN WO200270709-A2.
XX
PD 12-SEP-2002.
XX
PF 08-FEB-2002; 2002WO-US003709.
XX
PR 09-FEB-2001; 2001US-0268117P.
PR 15-FEB-2001; 2001US-0269618P.
PR 23-FEB-2001; 2001US-0271118P.
PR 07-MAR-2001; 2001US-0274486P.
PR 09-MAR-2001; 2001US-0274436P.
PR 28-NOV-2001; 2001US-0334229P.
PR 01-FEB-2002; 2002US-0353284P.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal PG, Baughn MR, Yao MG, Walia NK, Elliot VS, Xu Y;
PI Honchell CD, Yue H, Ding L, Gietzen KJ, Ison CH, Lu DAM;
PI Hafalia AJA, Ghandi AR, Thangavelu K, Sanjanwala MM, Tang YT;
PI Ramkumar J, Griffin JA, Swarnaker A, Azimzai Y, Sapperstein SK;
PI Burford N, Lee EA, Lu Y, Tran UK, Marquis JP;
XX
DR WPI; 2002-713453/77.
DR N-PSDB; AAL49942.
XX
PT New human molecules for disease detection and treatment (MDDT), useful
PT for diagnosing, treating and preventing diseases or conditions associated
PT with the aberrant MDDT expression, e.g. cancer, AIDS, asthma, diabetes,
PT hepatitis.
XX
PS Claim 1; Page 148-150; 177pp; English.
XX
CC The present invention relates to human proteins and coding sequences of
CC molecules for disease detection and treatment MDDT. The sequences can be
CC used in the treatment of diseases associated with the decreased
CC expression or overexpression of MDDT, such as cell proliferative (cancer,
CC atherosclerosis, hepatitis), autoimmune/inflammatory (e.g. AIDS,
CC allergies, Addison's disease, asthma), developmental (dwarfism, renal
CC tubular acidosis), neurological (e.g. stroke, Parkinson's disease,
CC epilepsy) and cardiovascular (congestive heart failure, myocardial
CC infarction, angina pectoris) disorders. The present sequence is a protein
CC of the invention
XX
SQ Sequence 667 AA;

Query Match 98.8%; Score 1048; DB 5; Length 667;
Best Local Similarity 99.0%; Pred. No. 1.3e-105;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200
```

RESULT 9
ADA54816
ID ADA54816 standard; protein; 667 AA.
XX
AC ADA54816;
XX
DT 20-NOV-2003 (first entry)

XX
DE Human protein, SEQ ID 2384.
XX
KW Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;
KW Gene Therapy; human; secretory protein; membrane proteins; cancer;
KW inflammatory disease; osteoporosis; neurological disease.
XX
OS Homo sapiens.
XX
PN EP1293569-A2.
XX
PD 19-MAR-2003.
XX
PF 21-MAR-2002; 2002EP-00006586.
XX
PR 14-SEP-2001; 2001JP-00328381.
PR 24-JAN-2002; 2002US-0350435P.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-395539/38.
DR N-PSDB; ADA53177.
XX
PT New polynucleotides encoding full-length polypeptides, e.g. secretory
PT and/or membrane proteins, useful for developing medicines for diseases in
PT which the gene is involved, or as target molecules for gene therapy.
XX
PS Claim 14; SEQ ID NO 2384; 205pp; English.
XX
CC The present invention relates to novel human secretory or membrane
CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-
CC ADA54071). The coding sequences are useful in the gene therapy of
CC diseases caused by abnormalities of the proteins, e.g. cancer,
CC inflammatory diseases, osteoporosis or neurological disease.
XX
SQ Sequence 667 AA;

Query Match 98.8%; Score 1048; DB 6; Length 667;
Best Local Similarity 99.0%; Pred. No. 1.3e-105;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200
```

RESULT 10
ABU80778
ID ABU80778 standard; protein; 667 AA.
XX
AC ABU80778;
XX
DT 23-JUN-2003 (first entry)
XX
DE Human PRO polypeptide #40.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003036635-A1.
XX
PD 20-FEB-2003.
XX
PF 28-AUG-2002; 2002US-00230163.
XX
PR 25-JUL-2000; 2000US-0220638P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-342045/32.
DR N-PSDB; ACA66880.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for the manufacture of a medicament for diagnosing or treating
PT tumor.
XX
PS Claim 11; Fig 80; 314pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
CC useful in diagnostic assays for PRO, by detecting its expression in
CC specific cells, tissues or serum, and for affinity purification of PRO
CC from recombinant cell culture or natural sources. ABU80739-ABU80860
CC represent the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 667 AA;

Query Match 98.8%; Score 1048; DB 6; Length 667;
Best Local Similarity 99.0%; Pred. No. 1.3e-105;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200
```

RESULT 11
ABO33744
ID ABO33744 standard; protein; 667 AA.
XX
AC ABO33744;
XX
DT 17-SEP-2003 (first entry)
XX

```
DE   Novel human secreted and transmembrane protein PRO10282.
XX
KW   Human; secreted and transmembrane protein; PRO; cytostatic;
KW   antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
KW   chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
KW   pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;
KW   colon tumour; breast tumour; prostate tumour; rectal tumour;
KW   liver tumour; bone disorder; cartilage disorder; sports injury;
KW   arthritis; wound.
XX
OS   Homo sapiens.
XX
PN   US2003045687-A1.
XX
PD   06-MAR-2003.
XX
PF   12-AUG-2002; 2002US-00218631.
XX
PR   01-JUN-2001; 2001WO-US017800.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-APR-2002; 2002US-00119480.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Desnoyers L,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Smith V,  Stephan JF,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-512315/48.
DR   N-PSDB; ACD68632.
XX
PT   New genes, and its encoded secreted and transmembrane polypeptides,
PT   useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
PT   pericyte proliferation, especially for treating lung tumors, arthritis or
PT   wounds in a mammal.
XX
PS   Claim 11; Fig 80; 314pp; English.
XX
CC   The invention describes an isolated nucleic acid molecule comprising a
CC   sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC   122 PRO (secreted and transmembrane) polypeptides whose sequences are
CC   fully defined in the specification; or (b) any of 122 nucleotide
CC   sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
CC   specification; or the full length coding sequence of any these 122
CC   nucleotide sequences. The PRO polypeptides or polynucleotides are useful
CC   as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC   particularly useful for detecting tumours (e.g. lung tumour, colon
CC   tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC   in a mammal, for stimulating the release of TNF-alpha from human blood,
CC   for stimulating the proliferation or differentiation of chondrocyte
CC   cells, for stimulating proliferation of pericyte cells, or for modulating
CC   normal human dermal fibroblast proliferation. The PRO nucleic acid or
CC   polypeptide is also useful for treating tumours or various bone and/or
CC   cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
CC   PRO polypeptides are useful in drug screening, particularly as targets
CC   for therapeutic intervention in these diseases, and in the diagnostic
CC   determination of the presence of these diseases. The PRO polypeptides are
CC   also useful as molecular weight markers, or for chromosome
CC   identification. The PRO genes are useful as hybridisation probes, or for
CC   screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC   also be used in gene therapy, particularly for replacing a defective
CC   gene. This is the amino acid sequence of a novel human secreted and
CC   transmembrane PRO polypeptide
XX
SQ   Sequence 667 AA;

  Query Match           98.8%;  Score 1048;  DB 6;  Length 667;
  Best Local Similarity  99.0%;  Pred. No. 1.3e-105;
  Matches  196;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200


RESULT 12
ABJ72267
ID   ABJ72267 standard; protein; 667 AA.
XX
AC   ABJ72267;
XX
DT   06-NOV-2003  (first entry)
XX
DE   Human PRO10282 protein.
XX
KW   PRO; proliferation; pericyte cell; TNF-alpha; blood; chondrocyte;
KW   differentiation; dermal fibroblast; tumour; gene therapy; cytostatic.
XX
OS   Homo sapiens.
XX
PN   US2003050448-A1.
XX
PD   13-MAR-2003.
XX
PF   28-AUG-2002; 2002US-00230414.
XX
PR   01-JUN-2001; 2001WO-US017800.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-APR-2002; 2002US-00119480.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Desnoyers L,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Smith V,  Stephan JF,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-521818/49.
DR   N-PSDB; ABT44265.
XX
PT   New nucleic acid encoding for a PRO protein, useful for the manufacture
PT   of a medicament for diagnosing or treating tumors or for measuring or
PT   detecting expression of an associated gene.
XX
PS   Claim 11; Fig 80; 315pp; English.
XX
CC   The invention relates to a novel isolated nucleic acid encoding a fully
CC   defined PRO polypeptide. The molecules of the invention may be useful for
CC   stimulating proliferation or gene expression in pericyte cells or the
CC   release of TNF-alpha from human blood. Other possible uses include the
CC   stimulation or inhibition of chondrocyte proliferation or
CC   differentiation, the stimulation of human dermal fibroblast cell
CC   proliferation and the detection of the presence of a tumour within a
CC   mammal. Furthermore, the nucleic acid may be useful for the manufacture
CC   of a medicament for diagnosing or treating a tumour within a mammal or
CC   for measuring or detecting the expression of an associated gene, as well
CC   as during gene therapy. The current sequence is that of the human PRO
CC   protein of the invention
XX
SQ   Sequence 667 AA;

  Query Match           98.8%;  Score 1048;  DB 6;  Length 667;
  Best Local Similarity  99.0%;  Pred. No. 1.3e-105;
  Matches  196;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
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```

```
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
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Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
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Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200
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RESULT 13
ABJ72395
ID ABJ72395 standard; protein; 667 AA.
XX
AC ABJ72395;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human PRO10282 protein.
XX
KW PRO; blood; proliferation; pericyte cell; TNF alpha; chondrocyte;
KW tumour necrosis factor; proliferation; differentiation; gene therapy;
KW dermal fibroblast.
XX
OS Homo sapiens.
XX
PN US2003027988-A1.
XX
PD 06-FEB-2003.
XX
PF 26-AUG-2002; 2002US-00227884.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-503301/47.
DR N-PSDB; ABT44548.
XX
PT New PRO protein encoding nucleic acid, useful for preparing PRO
PT polypeptides and anti-PRO antibodies for detecting the presence of a
PT tumor in a mammal.
XX
PS Claim 11; Fig 80; 324pp; English.
XX
CC The invention relates to a novel isolated PRO protein encoding nucleic
CC acid. The nucleic acid of the invention may be useful for preparing PRO
CC polypeptides and anti-PRO antibodies for detecting the presence of a
CC tumour in a mammal. Furthermore, the molecules of the invention may be
CC useful for stimulating proliferation or gene expression in pericyte
CC cells, the release of tumour necrosis factor (TNF)-alpha from human
CC blood, the proliferation or differentiation of chondrocyte cells and for
CC inhibiting the proliferation of normal human dermal fibroblast cells.
CC Finally, the molecules may be utilised during gene therapy. The current
CC sequence is that of the human PRO protein of the invention
XX
SQ Sequence 667 AA;

Query Match 98.8%; Score 1048; DB 6; Length 667;
Best Local Similarity 99.0%; Pred. No. 1.3e-105;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200
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RESULT 14
ABO34290
ID ABO34290 standard; protein; 667 AA.
XX
AC ABO34290;
XX
DT 19-SEP-2003 (first entry)
XX
DE Human secreted/transmembrane polypeptide PRO 10282.
XX
KW Human; chondrocyte stimulation; TNF-alpha stimulation; gene therapy;
KW human dermal fibroblast stimulation; tumour; tissue typing;
KW affinity purification.
XX
OS Homo sapiens.
XX
PN US2003044934-A1.
XX
PD 06-MAR-2003.
XX
PF 28-AUG-2002; 2002US-00230338.
XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-492274/46.
DR N-PSDB; ACD82215.
XX
PT New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX
PS Claim 19; Fig 80; 315pp; English.
XX
CC The invention relates to an isolated nucleic acid encoding a PRO
CC polypeptide. Nucleic acids that encode PRO can be used to generate either
CC transgenic animals or knock-out animals useful in developing and
CC screening of therapeutically useful reagents. The nucleic acids may also
CC be used in gene therapy for replacing defective gene, in chromosome
CC identification, as chromosome markers, or in generating probes to isolate
CC full length PRO cDNA. The PRO polypeptides are useful for chondrocyte
CC stimulation, TNF-alpha stimulation, human dermal fibroblasts stimulation
CC and for detecting the presence of tumour in an mammal. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis
CC and the isolated nucleic acids may be used for recombinantly expressing
CC those markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The present sequence represents the amino acid sequence
CC of a human secreted/transmembrane PRO polypeptide
XX

```
SQ   Sequence 667 AA;

  Query Match           98.8%;  Score 1048;  DB 6;  Length 667;
  Best Local Similarity  99.0%;  Pred. No. 1.3e-105;
  Matches  196;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
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Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200


RESULT 15
ABJ72097
ID   ABJ72097 standard; protein; 667 AA.
XX
AC   ABJ72097;
XX
DT   16-OCT-2003  (first entry)
XX
DE   Human membrane bound receptor/protein PRO10282 amino acid sequence.
XX
KW   Human; PRO; membrane bound protein; membrane bound receptor;
KW   cell proliferation; cell migration; cell differentiation;
KW   mitogenic factor; survival factor; cytotoxic factor;
KW   differentiation factor; neuropeptide; hormone; cell receptor;
KW   receptor-ligand interaction; cytostatic; chondrocyte; tumour.
XX
OS   Homo sapiens.
XX
PN   US2003065147-A1.
XX
PD   03-APR-2003.
XX
PF   29-AUG-2002; 2002US-00232224.
XX
PR   28-JUL-1999;   99US-0146222P.
PR   24-FEB-2000; 2000WO-US005004.
PR   02-MAR-2000; 2000WO-US005841.
PR   01-JUN-2001; 2001WO-US017800.
PR   29-JUN-2001; 2001WO-US021066.
PR   09-APR-2002; 2002US-00119480.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Baker KP,  Desnoyers L,  Gerritsen ME,  Goddard A,  Godowski PJ;
PI   Grimaldi JC,  Gurney AL,  Smith V,  Stephan JF,  Watanabe CK,  Wood WI;
XX
DR   WPI; 2003-522018/49.
DR   N-PSDB; ABT43921.
XX
PT   One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT   useful for the manufacture of a medicament for diagnosing or treating
PT   tumor.
XX
PS   Claim 11; Fig 80; 315pp; English.
XX
CC   This invention relates to one hundred and twenty two novel nucleic acids
CC   encoding human PRO membrane bound proteins or receptors. Extracellular
CC   proteins play important roles in the formation, differentiation and
CC   maintenance of multicellular organisms. The fate of many individual cells
CC   (for example proliferation, migration or differentiation) is typically
CC   governed by information received from other cells and the immediate
CC   environment. The information is often transmitted by secreted
CC   polypeptides (for example mitogenic factors, survival factors, cytotoxic
CC   factors, differentiation factors, neuropeptides and hormones) which are
CC   received and interpreted by diverse cell receptors or membrane bound
CC   proteins. These membrane bound proteins and receptors may be of use as
CC   pharmaceutical and diagnostic agents, such as in the blocking of receptor
CC   -ligand interactions. The current invention provides the amino acid
CC   sequences of novel human membrane bound receptors and proteins, along
CC   with the cDNA sequences encoding them. The novel proteins of the
CC   invention may have cytostatic activities through the stimulation of
CC   chondrocytes. The nucleic acids of the invention may be useful for the
CC   manufacture of a medicament for diagnosing or treating a tumour in a
CC   mammal. In addition, they may be useful for measuring or detecting the
CC   expression of a tumour associated gene. The present sequence is the amino
CC   acid sequence of a human PRO protein of the invention
XX
SQ   Sequence 667 AA;

  Query Match           98.8%;  Score 1048;  DB 7;  Length 667;
  Best Local Similarity  99.0%;  Pred. No. 1.3e-105;
  Matches  196;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
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Db        183 HLGVQVWQRAECPQVPKI 200


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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 13:30:00 ; Search time 23.5458 Seconds
(without alignments)
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Perfect score: 1061
Sequence: 1 MSQPAGNQTSPGATEDYSYG.....WAHLGVQVWQRAECPQVPKI 199

Scoring table: BLOSUM62
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Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	88	8.3	509	4	US-09-252-991A-21709	Sequence 21709, A
2	85.5	8.1	380	3	US-08-924-345-2	Sequence 2, Appli
3	84	7.9	913	4	US-09-140-378A-2	Sequence 2, Appli
4	84	7.9	919	1	US-08-336-343A-2	Sequence 2, Appli
5	84	7.9	937	4	US-09-949-016-8366	Sequence 8366, Ap
6	84	7.9	937	4	US-09-949-016-8367	Sequence 8367, Ap
7	84	7.9	937	4	US-09-949-016-8368	Sequence 8368, Ap
8	83	7.8	913	1	US-08-445-640-4	Sequence 4, Appli
9	83	7.8	913	3	US-08-170-558-4	Sequence 4, Appli
10	83	7.8	913	3	US-08-447-314-4	Sequence 4, Appli
11	83	7.8	913	3	US-08-445-461-4	Sequence 4, Appli
12	83	7.8	913	4	US-09-223-490-4	Sequence 4, Appli
13	81	7.6	429	4	US-09-252-991A-30376	Sequence 30376, A
14	80.5	7.6	463	4	US-09-252-991A-19381	Sequence 19381, A
15	80	7.5	433	3	US-09-106-075A-86	Sequence 86, Appl
16	80	7.5	699	5	PCT-US94-07297-39	Sequence 39, Appl
17	80	7.5	921	1	US-08-396-479B-2	Sequence 2, Appli
18	80	7.5	921	1	US-08-818-823-2	Sequence 2, Appli
19	80	7.5	1171	4	US-09-417-197-131	Sequence 131, App
20	80	7.5	1181	4	US-09-417-197-133	Sequence 133, App
21	79.5	7.5	435	4	US-09-902-540-14931	Sequence 14931, A
22	79	7.4	505	1	US-08-221-750A-5	Sequence 5, Appli
23	78.5	7.4	369	4	US-09-902-540-10817	Sequence 10817, A
24	78.5	7.4	532	4	US-09-949-016-6607	Sequence 6607, Ap
25	78.5	7.4	540	4	US-09-252-991A-22555	Sequence 22555, A
26	78.5	7.4	3519	3	US-09-428-517-4	Sequence 4, Appli
27	78	7.4	475	4	US-09-252-991A-25837	Sequence 25837, A
28	77.5	7.3	535	4	US-09-949-016-10290	Sequence 10290, A
29	76.5	7.2	875	1	US-08-785-241-5	Sequence 5, Appli
30	76	7.2	478	4	US-09-902-540-10474	Sequence 10474, A
31	75	7.1	331	2	US-08-986-217-7	Sequence 7, Appli
32	75	7.1	575	4	US-09-949-016-9760	Sequence 9760, Ap
33	74.5	7.0	337	4	US-09-252-991A-33066	Sequence 33066, A
34	74.5	7.0	482	4	US-09-252-991A-23559	Sequence 23559, A
35	74.5	7.0	657	4	US-09-902-540-12047	Sequence 12047, A
36	73.5	6.9	147	4	US-09-252-991A-29490	Sequence 29490, A
37	73.5	6.9	311	4	US-09-252-991A-30973	Sequence 30973, A
38	73.5	6.9	356	4	US-09-602-777A-424	Sequence 424, App
39	73.5	6.9	378	3	US-09-482-180A-2	Sequence 2, Appli
40	73.5	6.9	578	1	US-08-653-740-3	Sequence 3, Appli
41	73.5	6.9	578	2	US-09-073-594-3	Sequence 3, Appli
42	73.5	6.9	578	3	US-09-275-925-3	Sequence 3, Appli
43	73.5	6.9	636	1	US-08-653-740-5	Sequence 5, Appli
44	73.5	6.9	636	2	US-09-073-594-5	Sequence 5, Appli
45	73.5	6.9	636	3	US-09-275-925-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-252-991A-21709
; Sequence 21709, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21709
; LENGTH: 509
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21709

Query Match 8.3%; Score 88; DB 4; Length 509;
Best Local Similarity 27.3%; Pred. No. 0.3;
Matches 51; Conservative 13; Mismatches 65; Indels 58; Gaps 12;

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Qy          26 EPQGGXELQPEGEVPSCH-----TSIPPGLYHACLASLSILVLLLLAMLVRRRQLW---- 76
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Db         188 EPQPGGRLRAPGALPADHRGSVRPDFPP---HA--AGLS----------NRRHGAWRSPA 232

Qy          77 ---PDC--VRGRPGLPSPVDF------LAGDRPRAVPAAVFMVLLSSLCLLLPDEDALPF 125
                  :|  : | ||   |:|          |   |  | |       :|| :|   ||
Db         233 GATAECRMLAGLPGGHGPLDHRPVAGPAGGGTARRAPRAA-----GTLCRAVPRAAALSR 287

Qy         126 LTLASA----PSQDGKTEAPRGAW--------KILGLFHYAALYYP-----LAACATAGH 168
                 : :       :|  |   |||         :| | | |  :||     |   | ||
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Qy         169 TAAHLLG 175
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Db         347 TQARTGG 353
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RESULT 2
US-08-924-345-2
; Sequence 2, Application US/08924345
; Patent No. 6224878
; GENERAL INFORMATION:
; APPLICANT: LEUNG-TACK Patricia
; APPLICANT: LEGASTELOIS Isabelle, Christine, Marie-Andree

```
;    APPLICANT:  AUDONNET Jean-Christophe, Francis
;    APPLICANT:  RIVIERE Michel, Emile, Albert
;    TITLE OF INVENTION:  Mutants and vaccines of the Infectious
;    TITLE OF INVENTION:  Bovine Rhinotracheitis virus
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  LARSON AND TAYLOR
;      STREET:  727 SOUTH TWENTY-THIRD STREET
;      CITY:  ARLINGTON
;      STATE:  VIRGINIA
;      COUNTRY:  USA
;      ZIP:  22202
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25 (EPO)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/924,345
;      FILING DATE:  04-SEP-1997
;      CLASSIFICATION:  424
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/199,172
;      FILING DATE:  09-AUG-1994
;      APPLICATION NUMBER:  FR 92 07930
;      FILING DATE:  26-JUN-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  SARRO, THOMAS P.
;      REGISTRATION NUMBER:  19396
;      REFERENCE/DOCKET NUMBER:  XI
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 920-7200
;      TELEFAX:  (703) 892-8428
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  380 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-924-345-2

  Query Match             8.1%;  Score 85.5;  DB 3;  Length 380;
  Best Local Similarity   27.6%;  Pred. No. 0.38;
  Matches   37;  Conservative   12;  Mismatches   38;  Indels   47;  Gaps    6;

Qy          4 PAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLAS----LS 59
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Db        303 VLVLLLLALCAATVNCALRRRLLPCSRRVYKPRTCAACGSGTCAGRPPCRGAAPSAPATV 362

Qy         91 DFLAGDRPRAVPAA 104
                | | ||:| | |
Db        363 VAL-GSRPKAPPLA 375


RESULT 3
US-09-140-378A-2
; Sequence 2, Application US/09140378A
; Patent No. 6627733
; GENERAL INFORMATION:
;  APPLICANT: Johnson, Jeffrey D.
;  APPLICANT:  Rutter, William J.
;  APPLICANT:  Edman, Jeffrey C.
;  APPLICANT:  The Regents of the University of California
;  TITLE OF INVENTION: Receptor Tyrosine Kinase With a Discoidin-Type Binding
;  TITLE OF INVENTION:  Domain
;  FILE REFERENCE: 023070-079010US
;  CURRENT APPLICATION NUMBER: US/09/140,378A
;  CURRENT FILING DATE:  1998-08-26
;  PRIOR APPLICATION NUMBER: US 08/077,254
;  PRIOR FILING DATE: 1993-06-14
;  PRIOR APPLICATION NUMBER: US 08/292,299
;  PRIOR FILING DATE: 1994-08-16
;  NUMBER OF SEQ ID NOS: 6
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 913
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: discoidin domain receptor (DDR) tyrosine kinase
;   NAME/KEY: PEPTIDE
;   LOCATION: (1)..(18)
;   OTHER INFORMATION: signal peptide
;   NAME/KEY: SITE
;   LOCATION: (19)..(24)
;   OTHER INFORMATION: uncertain point of signal peptide cleavage between amino acids 19
;   NAME/KEY: DOMAIN
;   LOCATION: (31)..(185)
;   OTHER INFORMATION: discoidin I-type domain
;   NAME/KEY: SITE
;   LOCATION: (374)..(415)
;   OTHER INFORMATION: proline/glycine-rich portion of connecting region interrupted by
;   NAME/KEY: TRANSMEM
;   LOCATION: (417)..(439)
;   OTHER INFORMATION: transmembrane domain
;   NAME/KEY: SITE
;   LOCATION: (466)..(601)
;   OTHER INFORMATION: proline/glycine-rich portion of connecting region interrupted by
;   NAME/KEY: TURN
;   LOCATION: (510)..(513)
;   OTHER INFORMATION: tight turn recognition motif for internalization in coated pits
;   NAME/KEY: DOMAIN
;   LOCATION: (616)..(905)
;   OTHER INFORMATION: tyrosine kinase domain
US-09-140-378A-2

  Query Match             7.9%;  Score 84;  DB 4;  Length 913;
  Best Local Similarity   22.7%;  Pred. No. 1.9;
  Matches   39;  Conservative   20;  Mismatches   73;  Indels   40;  Gaps    7;

Qy          7 NQTSPGATEDYSYGSWYIDEPQ----GGXELQPEGEVPSCHT-SIPPGLYHACLASLSIL 61
              | :||      :    |:   |        ||:| |: |       |  :   || :: :|
Db        370 NNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILIGCLVAIILL 429

Qy         62 VLLLLAMLV-----------RRRQLWPD-----------CVRGRPGLPSPVDFL---- 93
              :||::|:::             || |  :            :  |||   |  :
Db        430 LLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREPPPYQEPRP 489

Qy         94 AGDRPRAVPAAVFMVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAW 145
              |: | : |     |   |  ||       |   | | |   |    |  ||
Db        490 RGNPPHSAPC----VPNGSALLLSNPAYRLLLATYARPPRGPG---PPTPAW 534


RESULT 4
US-08-336-343A-2
; Sequence 2, Application US/08336343A
; Patent No. 5677144
;  GENERAL INFORMATION:
;    APPLICANT:  Ullrich, Axel
;    APPLICANT:  Alves, Frauke
;    TITLE OF INVENTION:  CCK-2, A No. 5677144el Receptor Tyrosine Kinase
;    NUMBER OF SEQUENCES:  43
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Pennie & Edmonds
;      STREET:  1155 Avenue of the Americas
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.A.
;      ZIP:  10036-2711
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/336,343A
;      FILING DATE:  08-NOV-1994
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Coruzzi, Laura A.
;      REGISTRATION NUMBER:  30,742
;      REFERENCE/DOCKET NUMBER:  7683-065
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 790-9090
;      TELEFAX:  (212) 869-9741/8864
;      TELEX:  66141 PENNIE
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  919 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  protein
US-08-336-343A-2

  Query Match             7.9%;  Score 84;  DB 1;  Length 919;
  Best Local Similarity   22.7%;  Pred. No. 1.9;
  Matches   39;  Conservative   20;  Mismatches   73;  Indels   40;  Gaps    7;

Qy          7 NQTSPGATEDYSYGSWYIDEPQ----GGXELQPEGEVPSCHT-SIPPGLYHACLASLSIL 61
              | :||     :    |:   |        ||:| |: |       |  :   || :: :|
Db        370 NNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILIGCLVAIILL 429

Qy         62 VLLLLAMLV-----------RRRQLWPD-----------CVRGRPGLPSPVDFL---- 93
              :||::|:::           || |  :           :  |||   |  :
Db        430 LLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREPPPYQEPRP 489

Qy         94 AGDRPRAVPAAVFMVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAW 145
              |: | : |     |   | ||       |   | | |   |    |  ||
Db        490 RGNPPHSAPC----VPNGSALLLSNPAYRLLLATYARPPRGPG---PPTPAW 534


RESULT 5
US-09-949-016-8366
; Sequence 8366, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8366
;   LENGTH: 937
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-8366

  Query Match             7.9%;  Score 84;  DB 4;  Length 937;
  Best Local Similarity   22.7%;  Pred. No. 1.9;
  Matches   39;  Conservative   20;  Mismatches   73;  Indels   40;  Gaps    7;

Qy          7 NQTSPGATEDYSYGSWYIDEPQ----GGXELQPEGEVPSCHT-SIPPGLYHACLASLSIL 61
              | :||     :    |:   |        ||:| |: |       |  :   || :: :|
Db        394 NNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILIGCLVAIILL 453

Qy         62 VLLLLAMLV-----------RRRQLWPD-----------CVRGRPGLPSPVDFL----. 93
```

```
              :||::|:::           || |  :           :  |||   |  :
Db        454 LLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREPPPYQEPRP 513

Qy         94 AGDRPRAVPAAVFMVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAW 145
              |: | : |     |   | ||       |   | | |   |    |  ||
Db        514 RGNPPHSAPC----VPNGSALLLSNPAYRLLLATYARPPRGPG---PPTPAW 558


RESULT 6
US-09-949-016-8367
; Sequence 8367, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8367
;   LENGTH: 937
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-8367

  Query Match             7.9%;  Score 84;  DB 4;  Length 937;
  Best Local Similarity   22.7%;  Pred. No. 1.9;
  Matches   39;  Conservative   20;  Mismatches   73;  Indels   40;  Gaps    7;

Qy          7 NQTSPGATEDYSYGSWYIDEPQ----GGXELQPEGEVPSCHT-SIPPGLYHACLASLSIL 61
              | :||     :    |:   |        ||:| |: |       |  :   || :: :|
Db        394 NNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILIGCLVAIILL 453

Qy         62 VLLLLAMLV-----------RRRQLWPD-----------CVRGRPGLPSPVDFL---- 93
              :||::|:::           || |  :           :  |||   |  :
Db        454 LLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREPPPYQEPRP 513

Qy         94 AGDRPRAVPAAVFMVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAW 145
              |: | : |     |   | ||       |   | | |   |    |  ||
Db        514 RGNPPHSAPC----VPNGSALLLSNPAYRLLLATYARPPRGPG---PPTPAW 558


RESULT 7
US-09-949-016-8368
; Sequence 8368, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8368
;   LENGTH: 937
;   TYPE: PRT
;   ORGANISM: Human
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US-09-949-016-8368

  Query Match             7.9%;  Score 84;  DB 4;  Length 937;
  Best Local Similarity   22.7%;  Pred. No. 1.9;
  Matches   39;  Conservative   20;  Mismatches   73;  Indels   40;  Gaps    7;

Qy          7 NQTSPGATEDYSYGSWYIDEPQ----GGXELQPEGEVPSCHT-SIPPGLYHACLASLSIL 61
              | :||     :    |:   |        ||:| |: |       |  :   || :: :|
Db        394 NNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILIGCLVAIILL 453

Qy         62 VLLLLAMLV-----------RRRQLWPD-----------CVRGRPGLPSPVDFL---- 93
              :||::|:::           || |  :           :  |||   |  :
Db        454 LLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREPPPYQEPRP 513

Qy         94 AGDRPRAVPAAVFMVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAW 145
              |: | : |     |   | ||      |   | | |   |    |  ||
Db        514 RGNPPHSAPC----VPNGSALLLSNPAYRLLLATYARPPRGPG---PPTPAW 558


RESULT 8
US-08-445-640-4
; Sequence 4, Application US/08445640
; Patent No. 5709858
;  GENERAL INFORMATION:
;    APPLICANT:  Godowski, Paul J.
;    APPLICANT:  Mark, Melanie R.
;    APPLICANT:  Scadden, David T.
;    APPLICANT:  Baker, Kevin P.
;    APPLICANT:  Baron, Will F.
;    TITLE OF INVENTION:  Protein Tyrosine Kinases
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/445,640
;      FILING DATE:  22-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/170558
;      FILING DATE:  20-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/157563
;      FILING DATE:  23-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  854C2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-445-640-4

  Query Match             7.8%;  Score 83;  DB 1;  Length 913;
  Best Local Similarity   22.7%;  Pred. No. 2.4;
  Matches   39;  Conservative   20;  Mismatches   73;  Indels   40;  Gaps    7;

Qy          7 NQTSPGATEDYSYGSWYIDEPQ----GGXELQPEGEVPSCH-TSIPPGLYHACLASLSIL 61
              | :||     :    |:   |        ||:| |: |       |  :   || :: :|
Db        370 NNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKPEGSPTAILIGCLVAIILL 429

Qy         62 VLLLLAMLV-----------RRRQLWPD-----------CVRGRPGLPSPVDFL---- 93
              :||::|:::           || |  :           :  |||   |  :
Db        430 LLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREPPPYQEPRP 489

Qy         94 AGDRPRAVPAAVFMVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAW 145
              |: | : |     |   | ||      |   | | |   |    |  ||
Db        490 RGNPPHSAPC----VPNGSALLLSNPAYRLLLATYARPPRGPG---PPTPAW 534


RESULT 9
US-08-170-558-4
; Sequence 4, Application US/08170558
; Patent No. 6001621
;  GENERAL INFORMATION:
;    APPLICANT:  Godowski, Paul J.
;    APPLICANT:  Mark, Melanie R.
;    APPLICANT:  Scadden, David T.
;    APPLICANT:  Baker, Kevin P.
;    APPLICANT:  Baron, Will F.
;    TITLE OF INVENTION:  Protein Tyrosine Kinases
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/170,558
;      FILING DATE:  20-DEC-1993
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/157563
;      FILING DATE:  23-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  854C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-170-558-4

  Query Match             7.8%;  Score 83;  DB 3;  Length 913;
  Best Local Similarity   22.7%;  Pred. No. 2.4;
  Matches   39;  Conservative   20;  Mismatches   73;  Indels   40;  Gaps    7;

Qy          7 NQTSPGATEDYSYGSWYIDEPQ----GGXELQPEGEVPSCH-TSIPPGLYHACLASLSIL 61
              | :||     :    |:   |        ||:| |: |       |  :   || :: :|
Db        370 NNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKPEGSPTAILIGCLVAIILL 429

Qy         62 VLLLLAMLV-----------RRRQLWPD-----------CVRGRPGLPSPVDFL---- 93
              :||::|:::           || |  :           :  |||   |  :
Db        430 LLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREPPPYQEPRP 489

Qy         94 AGDRPRAVPAAVFMVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAW 145
              |: | : |     |   | ||      |   | | |   |    |  ||
Db        490 RGNPPHSAPC----VPNGSALLLSNPAYRLLLATYARPPRGPG---PPTPAW 534
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```
RESULT 10
US-08-447-314-4
; Sequence 4, Application US/08447314
; Patent No. 6087144
;  GENERAL INFORMATION:
;    APPLICANT:  Scadden, David T.
;    APPLICANT:  Baker, Kevin P.
;    APPLICANT:  Baron, Will F.
;    TITLE OF INVENTION:  Protein Tyrosine Kinases
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/447,314
;      FILING DATE:  22-MAY-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/170558
;      FILING DATE:  20-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/157563
;      FILING DATE:  23-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  854C1D2
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-447-314-4

  Query Match             7.8%;  Score 83;  DB 3;  Length 913;
  Best Local Similarity   22.7%;  Pred. No. 2.4;
  Matches   39;  Conservative   20;  Mismatches   73;  Indels   40;  Gaps    7;

Qy          7 NQTSPGATEDYSYGSWYIDEPQ----GGXELQPEGEVPSCH-TSIPPGLYHACLASLSIL 61
              | :||     :    |:   |        ||:| |: |       |  :   || :: :|
Db        370 NNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKPEGSPTAILIGCLVAIILL 429

Qy         62 VLLLLAMLV-----------RRRQLWPD-----------CVRGRPGLPSPVDFL---- 93
              :||::|:::             || |  :            :  |||   |  :
Db        430 LLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREPPPYQEPRP 489

Qy         94 AGDRPRAVPAAVFMVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAW 145
               |: | : |     |   |  ||       |   | | |   |    |  ||
Db        490 RGNPPHSAPC----VPNGSALLLSNPAYRLLLATYARPPRGPG---PPTPAW 534


RESULT 11
US-08-445-461-4
; Sequence 4, Application US/08445461
; Patent No. 6096527
;  GENERAL INFORMATION:
;    APPLICANT:  Godowski, Paul J.
;    APPLICANT:  Mark, Melanie R.
;    APPLICANT:  Scadden, David T.
;    APPLICANT:  Baker, Kevin P.
;    APPLICANT:  Baron, Will F.
;    TITLE OF INVENTION:  Protein Tyrosine Kinases
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
;      STREET:  460 Point San Bruno Blvd
;      CITY:  South San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94080
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  patin (Genentech)
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/445,461
;      FILING DATE:  22-MAY-1995
;      CLASSIFICATION:  530
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/170558
;      FILING DATE:  20-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/157563
;      FILING DATE:  23-NOV-1993
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hasak, Janet E.
;      REGISTRATION NUMBER:  28,616
;      REFERENCE/DOCKET NUMBER:  854C3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415/225-1896
;      TELEFAX:  415/952-9881
;      TELEX:  910/371-7168
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  913 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
US-08-445-461-4

  Query Match             7.8%;  Score 83;  DB 3;  Length 913;
  Best Local Similarity   22.7%;  Pred. No. 2.4;
  Matches   39;  Conservative   20;  Mismatches   73;  Indels   40;  Gaps    7;

Qy          7 NQTSPGATEDYSYGSWYIDEPQ----GGXELQPEGEVPSCH-TSIPPGLYHACLASLSIL 61
              | :||     :    |:   |        ||:| |: |       |  :   || :: :|
Db        370 NNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKPEGSPTAILIGCLVAIILL 429

Qy         62 VLLLLAMLV-----------RRRQLWPD-----------CVRGRPGLPSPVDFL---- 93
              :||::|:::             || |  :            :  |||   |  :
Db        430 LLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREPPPYQEPRP 489

Qy         94 AGDRPRAVPAAVFMVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAW 145
               |: | : |     |   |  ||       |   | | |   |    |  ||
Db        490 RGNPPHSAPC----VPNGSALLLSNPAYRLLLATYARPPRGPG---PPTPAW 534


RESULT 12
US-09-223-490-4
; Sequence 4, Application US/09223490
; Patent No. 6825324
;  GENERAL INFORMATION:
;    APPLICANT:  Godowski, Paul J.
;    APPLICANT:  Mark, Melanie R.
;    APPLICANT:  Scadden, David T.
;    APPLICANT:  Baker, Kevin P.
;    APPLICANT:  Baron, Will F.
;    TITLE OF INVENTION:  Protein Tyrosine Kinases
;    NUMBER OF SEQUENCES:  35
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Genentech, Inc.
```

```
;       STREET:  460 Point San Bruno Blvd
;       CITY:  South San Francisco
;       STATE:  California
;       COUNTRY:  USA
;       ZIP:  94080
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  5.25 inch, 360 Kb floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  patin (Genentech)
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/09/223,490
;       FILING DATE:
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  08/170,558
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Hasak, Janet E.
;       REGISTRATION NUMBER:  28,616
;       REFERENCE/DOCKET NUMBER:  854C1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  415/225-1896
;       TELEFAX:  415/952-9881
;       TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  913 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-09-223-490-4

  Query Match             7.8%;  Score 83;  DB 4;  Length 913;
  Best Local Similarity   22.7%;  Pred. No. 2.4;
  Matches   39;  Conservative   20;  Mismatches   73;  Indels   40;  Gaps    7;

Qy          7 NQTSPGATEDYSYGSWYIDEPQ----GGXELQPEGEVPSCH-TSIPPGLYHACLASLSIL 61
              | :||     :    |:   |       ||:| |: |     |  :   || :: :|
Db        370 NNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKPEGSPTAILIGCLVAIILL 429

Qy         62 VLLLLAMLV-----------RRRQLWPD-----------CVRGRPGLPSPVDFL---- 93
              :||::|:::           || |  :           :  |||   |  :
Db        430 LLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREPPPYQEPRP 489

Qy         94 AGDRPRAVPAAVFMVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAW 145
              |: | : |     |  | ||      |  | | |  |   |  ||
Db        490 RGNPPHSAPC----VPNGSALLLSNPAYRLLLATYARPPRGPG---PPTPAW 534


RESULT 13
US-09-252-991A-30376
; Sequence 30376, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 30376
;   LENGTH: 429
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30376

  Query Match             7.6%;  Score 81;  DB 4;  Length 429;
  Best Local Similarity   30.4%;  Pred. No. 1.5;
  Matches   56;  Conservative    8;  Mismatches   70;  Indels   50;  Gaps    9;

Qy         33 LQPEGEVPSCHTSIPPGLYHACLASLSILVLLLLAMLVRRR---QLWPD----CVRGRPG 85
              | ||   |  |   ||    :  |  :|         ||||   |||||     :||:|
Db         83 LHPERHQPDRHRRFPP--VRSQRAERTIDGGHRPVRPVRRRTSLQLWPDREERGIRGKPQ 140

Qy         86 LPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDEDALP------FLTLASAPSQDGKTE 139
                    | | :| |  |                ||   |        ||   | | | |  :
Db        141 -------LGGIQPAAGSA------------LPRRQADHRQRRGLFL---SHPGQAGAPD 177

Qy        140 AP---------RGAWKILGLFHYAALYYPLAACA---TAGHTAAHLLGSTLSWAHLGVQV 187
               |         |      | |  |||  | |  |    :|  || | || |   ||
Db        178 VPHLPAGGEAGRYPHPPPGAFRPAALRQPAADPAPGRASGAAAALLEGSRLPRHHLHRAA 237

Qy        188 WQRA 191
               ||:
Db        238 GQRS 241


RESULT 14
US-09-252-991A-19381
; Sequence 19381, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 19381
;   LENGTH: 463
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19381

  Query Match             7.6%;  Score 80.5;  DB 4;  Length 463;
  Best Local Similarity   29.0%;  Pred. No. 1.8;
  Matches   54;  Conservative   14;  Mismatches   57;  Indels   61;  Gaps   13;

Qy         27 PQGGXELQPEGEVPSCHTSIPPGLYHACLASLSILVLLLLAMLVRRRQLWPDCVRGRP-- 84
              | ||   |   |  |              |  |:|::|:  | |::|     ||:    ||
Db        226 PLGGQWLADLGGHP------------AVFATLAVLLASLAALVV---PAWPET---RPLL 267

Qy         85 -GLPSPVDF-----LAGDRP---RAVPAAVFMVLLSSLC----LLLPDEDALPF----LT 127
               | | |         :  |||   ||:  ||  ||: |       :: |   | |    |
Db        268 AGTPEPATLAIFRRVLADRPLQTRALLVAVLNVLVFSFYAAGPFMVGDLPGLGFGWIGLA 327

Qy        128 LASAPSQDG--KTEAPRGAWKI-----LGLFHYAALYYPLAACATAGHTAAHLLGST--- 177
              :| | |          ||  |       |||             | | || ||  || :
Db        328 IAIAGSLGALLNRRLPR-TWNSARRVRLGL----------ALAAAGATAQTLLAAVGYA 375

Qy        178 --LSWA 181
                 | ||
Db        376 EGLYWA 381


RESULT 15
US-09-106-075A-86
; Sequence 86, Application US/09106075A
; Patent No. 6316250
; GENERAL INFORMATION:
;  APPLICANT:  Hjelle MD, Brian
;  APPLICANT:  Jenison, Steve
;  TITLE OF INVENTION:  Molecular Clones Producing Recombinant DNA Antigens of
;  TITLE OF INVENTION:  the HARDS Virus.
;  FILE REFERENCE:  10312-8U1, Hjelle et al. (210312.0009)
;  CURRENT APPLICATION NUMBER: US/09/106,075A
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; CURRENT FILING DATE: 1998-06-29
; PRIOR APPLICATION NUMBER: 08/210,762
; PRIOR FILING DATE: 1994-03-22
; PRIOR APPLICATION NUMBER: 08/141,035
; PRIOR FILING DATE: 1993-10-26
; PRIOR APPLICATION NUMBER: 08/120,096
; PRIOR FILING DATE: 1993-09-13
; PRIOR APPLICATION NUMBER: 08/111,519
; PRIOR FILING DATE: 1993-08-25
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 86
; LENGTH: 433
; TYPE: PRT
; ORGANISM: Prospect Hill virus
US-09-106-075A-86

Query Match 7.5%; Score 80; DB 3; Length 433;
Best Local Similarity 24.1%; Pred. No. 1.9;
Matches 35; Conservative 21; Mismatches 55; Indels 34; Gaps 6;

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Qy         23 YIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSILVLLL----LAMLVRRRQLWPD 78
              |:  |     :: |   |    :|  ||: | : : :|:  ::     |  |:   | |
Db        178 YVSMPTAQSTMKAEELTPGRFRTIVCGLFPAQIMARNIISPVMGVIGFAFFVKD---WAD 234

Qy         79 CVRG-------------RPGLPS-PVDFLAGDRPRAVPAAVFMVLLSSLCLL----LPDE 120
               |:              ||| |:   :||:  |           |::   :|    |||
Db        235 KVKAFLDQKCPFLKAEPRPGQPAGEAEFLSSIR---------AYLMNRQAVLDETHLPDI 285

Qy        121 DALPFLTLASAPSQDGKTEAPRGAW 145
              |||  |  : -|:     | |  ||
Db        286 DALVELAASGDPTLPDSLENPHAAW 310
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Search completed: February 8, 2005, 13:42:10
Job time : 24.5458 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 13:32:20 ; Search time 66.4599 Seconds
(without alignments)
975.246 Million cell updates/sec

Title: US-09-816-653A-2
Perfect score: 1061
Sequence: 1 MSQPAGNQTSPGATEDYSYG.....WAHLGVQVWQRAECPQVPKI 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1059	99.8	199	10	US-09-816-653A-2	Sequence 2, Appli
2	1048	98.8	487	16	US-10-362-240-2	Sequence 2, Appli
3	1048	98.8	667	9	US-09-759-056-2	Sequence 2, Appli
4	1048	98.8	667	9	US-09-901-812-2	Sequence 2, Appli
5	1048	98.8	667	10	US-09-863-776-67	Sequence 67, Appl
6	1048	98.8	667	14	US-10-227-884-80	Sequence 80, Appl
7	1048	98.8	667	14	US-10-230-163-80	Sequence 80, Appl
8	1048	98.8	667	14	US-10-230-338-80	Sequence 80, Appl
9	1048	98.8	667	14	US-10-218-631-80	Sequence 80, Appl
10	1048	98.8	667	14	US-10-230-414-80	Sequence 80, Appl
11	1048	98.8	667	14	US-10-232-224-80	Sequence 80, Appl
12	1048	98.8	667	14	US-10-216-159A-80	Sequence 80, Appl
13	1048	98.8	667	14	US-10-218-849-80	Sequence 80, Appl
14	1048	98.8	667	14	US-10-227-873-80	Sequence 80, Appl
15	1048	98.8	667	14	US-10-227-883-80	Sequence 80, Appl
16	1048	98.8	667	14	US-10-219-076-80	Sequence 80, Appl
17	1048	98.8	667	14	US-10-230-434-80	Sequence 80, Appl
18	1048	98.8	667	14	US-10-219-003-80	Sequence 80, Appl
19	1048	98.8	667	14	US-10-219-075-80	Sequence 80, Appl
20	1048	98.8	667	14	US-10-219-464-80	Sequence 80, Appl
21	1048	98.8	667	14	US-10-219-466-80	Sequence 80, Appl
22	1048	98.8	667	14	US-10-219-479-80	Sequence 80, Appl
23	1048	98.8	667	14	US-10-219-481-80	Sequence 80, Appl
24	1048	98.8	667	14	US-10-230-260-80	Sequence 80, Appl
25	1048	98.8	667	14	US-10-232-231-80	Sequence 80, Appl
26	1048	98.8	667	14	US-10-232-233-80	Sequence 80, Appl
27	1048	98.8	667	14	US-10-216-165-80	Sequence 80, Appl
28	1048	98.8	667	14	US-10-218-956-80	Sequence 80, Appl
29	1048	98.8	667	14	US-10-219-468-80	Sequence 80, Appl
30	1048	98.8	667	14	US-10-219-478-80	Sequence 80, Appl
31	1048	98.8	667	14	US-10-219-536-80	Sequence 80, Appl
32	1048	98.8	667	14	US-10-233-205-80	Sequence 80, Appl
33	1048	98.8	667	14	US-10-219-072-80	Sequence 80, Appl
34	1048	98.8	667	14	US-10-219-470-80	Sequence 80, Appl
35	1048	98.8	667	14	US-10-219-474-80	Sequence 80, Appl
36	1048	98.8	667	14	US-10-219-524-80	Sequence 80, Appl
37	1048	98.8	667	14	US-10-219-528-80	Sequence 80, Appl
38	1048	98.8	667	14	US-10-227-880-80	Sequence 80, Appl
39	1048	98.8	667	14	US-10-227-881-80	Sequence 80, Appl
40	1048	98.8	667	14	US-10-227-882-80	Sequence 80, Appl
41	1048	98.8	667	14	US-10-230-436-80	Sequence 80, Appl
42	1048	98.8	667	14	US-10-232-223-80	Sequence 80, Appl
43	1048	98.8	667	14	US-10-232-225-80	Sequence 80, Appl
44	1048	98.8	667	14	US-10-232-227-80	Sequence 80, Appl
45	1048	98.8	667	14	US-10-232-229-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-09-816-653A-2
; Sequence 2, Application US/09816653A
; Publication No. US20030021788A1
; GENERAL INFORMATION:
; APPLICANT: Rastelli, Luca
; APPLICANT: Pennica, Diane
; TITLE OF INVENTION: NOVEL HUMAN STRA6-LIKE PROTEIN AND NUCLEIC ACIDS ENCODING THE SA
; FILE REFERENCE: 10716/57
; CURRENT APPLICATION NUMBER: US/09/816,653A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/191,532
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens hSTRA6 amino terminal polypeptide fragment
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (31)..(31)
; OTHER INFORMATION: Xaa is any amino acid
US-09-816-653A-2

Query Match 99.8%; Score 1059; DB 10; Length 199;
Best Local Similarity 100.0%; Pred. No. 1.4e-96;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 MSQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSI 60
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Db          1 MSQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSI 60

Qy         61 LVLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LVLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDE 120
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Qy        121 DALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSW 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 DALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSW 180

Qy        181 AHLGVQVWQRAECPQVPKI 199
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Db        181 AHLGVQVWQRAECPQVPKI 199
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RESULT 2
US-10-362-240-2
; Sequence 2, Application US/10362240
; Publication No. US20040185442A1
; GENERAL INFORMATION:
; APPLICANT: MAO, Yumin
; APPLICANT: XIE, Yi
; TITLE OF INVENTION: A NOVEL POLYPEPTIDE - HUMAN RETINOIC ACID-RESPONSIVE PROTEIN 53.5
; TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING THE SAME
; FILE REFERENCE: 011241.52054US
; CURRENT APPLICATION NUMBER: US/10/362,240
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/CN01/01252
; PRIOR FILING DATE: 2001-08-20
; PRIOR APPLICATION NUMBER: 00119715.0
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-362-240-2

Query Match 98.8%; Score 1048; DB 16; Length 487;
Best Local Similarity 99.0%; Pred. No. 5e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
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Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
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Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

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Db        183 HLGVQVWQRAECPQVPKI 200
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RESULT 3
US-09-759-056-2
; Sequence 2, Application US/09759056
; Patent No. US20020156252A1
; GENERAL INFORMATION:
; APPLICANT: Pennica, Diane
; APPLICANT: Smith, Victoria
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: No. US20020156252A1el STRA6 Polypeptides
; FILE REFERENCE: GENENT.2827A2
; CURRENT APPLICATION NUMBER: US/09/759,056
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/197089
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/175849
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/228914
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-759-056-2

Query Match 98.8%; Score 1048; DB 9; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
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Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200
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RESULT 4
US-09-901-812-2
; Sequence 2, Application US/09901812
; Patent No. US20020173461A1
; GENERAL INFORMATION:
; APPLICANT: Pennica, Diane
; APPLICANT: Polakis, Paul
; APPLICANT: Szeto, Wayne
; TITLE OF INVENTION: UPREGULATION OF TUMOR ANTIGENS TO
; TITLE OF INVENTION: ENHANCE EFFICACY OF IMMUNOTHERAPY
; FILE REFERENCE: GENENT.083A
; CURRENT APPLICATION NUMBER: US/09/901,812
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/228,914
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 09/759,056
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/175,849
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/197,089
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-901-812-2

Query Match 98.8%; Score 1048; DB 9; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
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Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
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Qy        182 HLGVQVWQRAECPQVPKI 199
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Db        183 HLGVQVWQRAECPQVPKI 200
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RESULT 5
US-09-863-776-67
; Sequence 67, Application US/09863776
; Publication No. US20030198953A1
; GENERAL INFORMATION:
;  APPLICANT: Spytek, Kimberly A
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Mishra, Vishnu
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Spaderna, Steven K
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Li, Li
;  APPLICANT:  Taupier, Raymond J
;  APPLICANT:  Gangolli, Esha
;  TITLE OF INVENTION: No. US20030198953A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-020
;  CURRENT APPLICATION NUMBER: US/09/863,776
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: 09/540,763
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 60/206,679
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: 60/206,688
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: 60/206,829
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: 60/207,748
;  PRIOR FILING DATE: 2000-05-30
;  PRIOR APPLICATION NUMBER: 60/207,798
;  PRIOR FILING DATE: 2000-05-30
;  PRIOR APPLICATION NUMBER: 60/208,263
;  PRIOR FILING DATE: 2000-05-31
;  PRIOR APPLICATION NUMBER: 60/208,831
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: 60/209,451
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: 60/210,060
;  PRIOR FILING DATE: 2000-06-07
;  PRIOR APPLICATION NUMBER: 60/219,507
;  PRIOR FILING DATE: 2000-07-20
;  PRIOR APPLICATION NUMBER: 60/221,337
;  PRIOR FILING DATE: 2000-07-26
;  PRIOR APPLICATION NUMBER: 60/221,927
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: 60/263,135
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: 60/263,688
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/263,694
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 155
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
;   LENGTH: 667
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-863-776-67

  Query Match             98.8%;  Score 1048;  DB 10;  Length 667;
  Best Local Similarity   99.0%;  Pred. No. 7.3e-95;
  Matches  196;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
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Qy        182 HLGVQVWQRAECPQVPKI 199
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Db        183 HLGVQVWQRAECPQVPKI 200
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RESULT 6
US-10-227-884-80
; Sequence 80, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Gerritsen, Mary
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stephan, Jean-Philippe F.
;  APPLICANT:  Watanabe, Colin L.
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3530P1C79
;  CURRENT APPLICATION NUMBER: US/10/227,884
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: 10/119,480
;  PRIOR FILING DATE: 2002-04-09
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/062287
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;  PRIOR FILING DATE: 1997-10-31
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;  PRIOR FILING DATE: 1998-04-15
;  PRIOR APPLICATION NUMBER: 60/082804
;  PRIOR FILING DATE: 1998-04-22
;  PRIOR APPLICATION NUMBER: 60/084441
;  PRIOR FILING DATE: 1998-05-06
;  PRIOR APPLICATION NUMBER: 60/085323
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/085579
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;  PRIOR APPLICATION NUMBER: 60/086392
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: 60/089532
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: 60/089538
;  PRIOR FILING DATE: 1998-06-17
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; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 98.8%; Score 1048; DB 14; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;

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  Matches  196;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
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Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
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Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
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Db        183 HLGVQVWQRAECPQVPKI 200


RESULT 7
US-10-230-163-80
; Sequence 80, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Gerritsen, Mary
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stephan, Jean-Philippe F.
;  APPLICANT:  Watanabe, Colin L.
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3530P1C96
;  CURRENT APPLICATION NUMBER: US/10/230,163
;  CURRENT FILING DATE:  2002-08-28
;  PRIOR APPLICATION NUMBER: 10/119,480
;  PRIOR FILING DATE: 2002-04-09
;  PRIOR APPLICATION NUMBER: 60/059113
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;  PRIOR APPLICATION NUMBER: 60/062287
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; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 98.8%; Score 1048; DB 14; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              |||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200
```

RESULT 8
US-10-230-338-80
; Sequence 80, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C92
; CURRENT APPLICATION NUMBER: US/10/230,338
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-80

Query Match 98.8%; Score 1048; DB 14; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200
```

RESULT 9
US-10-218-631-80
; Sequence 80, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C14
; CURRENT APPLICATION NUMBER: US/10/218,631
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-218-631-80

Query Match 98.8%; Score 1048; DB 14; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              ||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200
```

RESULT 10
US-10-230-414-80
; Sequence 80, Application US/10230414
; Publication No. US20030050448A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C98
; CURRENT APPLICATION NUMBER: US/10/230,414
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-414-80

Query Match 98.8%; Score 1048; DB 14; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
```

```
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200
```

RESULT 11
US-10-232-224-80
; Sequence 80, Application US/10232224
; Publication No. US20030065147A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C111
; CURRENT APPLICATION NUMBER: US/10/232,224
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-232-224-80

Query Match 98.8%; Score 1048; DB 14; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
```

```
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200
```

RESULT 12
US-10-216-159A-80
; Sequence 80, Application US/10216159A
; Publication No. US20030069397A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-159A-80

Query Match 98.8%; Score 1048; DB 14; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122
```

```
Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200


RESULT 13
US-10-218-849-80
; Sequence 80, Application US/10218849
; Publication No. US20030073814A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Gerritsen, Mary
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stephan, Jean-Philippe F.
;  APPLICANT:  Watanabe, Colin L.
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3530P1C11
;  CURRENT APPLICATION NUMBER: US/10/218,849
;  CURRENT FILING DATE:  2002-08-12
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
;   LENGTH: 667
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-218-849-80

  Query Match             98.8%;  Score 1048;  DB 14;  Length 667;
  Best Local Similarity   99.0%;  Pred. No. 7.3e-95;
  Matches  196;  Conservative    1;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              ||||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        183 HLGVQVWQRAECPQVPKI 200


RESULT 14
US-10-227-873-80
; Sequence 80, Application US/10227873
; Publication No. US20030073816A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Gerritsen, Mary
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stephan, Jean-Philippe F.
;  APPLICANT:  Watanabe, Colin L.
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3530P1C72
;  CURRENT APPLICATION NUMBER: US/10/227,873
;  CURRENT FILING DATE:  2002-08-26
;  PRIOR APPLICATION NUMBER: 10/119,480
;  PRIOR FILING DATE: 2002-04-09
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/062287
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063549
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/064103
;  PRIOR FILING DATE: 1997-10-31
;  PRIOR APPLICATION NUMBER: 60/069873
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: 60/078910
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/079294
;  PRIOR FILING DATE: 1998-03-25
;  PRIOR APPLICATION NUMBER: 60/079656
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: 60/079728
;  PRIOR FILING DATE: 1998-03-27
;  PRIOR APPLICATION NUMBER: 60/081819
;  PRIOR FILING DATE: 1998-04-15
;  PRIOR APPLICATION NUMBER: 60/081955
;  PRIOR FILING DATE: 1998-04-15
;  PRIOR APPLICATION NUMBER: 60/082804
;  PRIOR FILING DATE: 1998-04-22
;  PRIOR APPLICATION NUMBER: 60/084441
;  PRIOR FILING DATE: 1998-05-06
;  PRIOR APPLICATION NUMBER: 60/085323
;  PRIOR FILING DATE: 1998-05-13
;  PRIOR APPLICATION NUMBER: 60/085579
;  PRIOR FILING DATE: 1998-05-15
;  PRIOR APPLICATION NUMBER: 60/086392
;  PRIOR FILING DATE: 1998-05-22
;  PRIOR APPLICATION NUMBER: 60/089532
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: 60/089538
;  PRIOR FILING DATE: 1998-06-17
;  PRIOR APPLICATION NUMBER: 60/089905
;  PRIOR FILING DATE: 1998-06-18
;  PRIOR APPLICATION NUMBER: 60/090472
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090557
;  PRIOR FILING DATE: 1998-06-24
;  PRIOR APPLICATION NUMBER: 60/090691
;  PRIOR FILING DATE: 1998-06-25
;  PRIOR APPLICATION NUMBER: 60/090695
;  PRIOR FILING DATE: 1998-06-25
;  PRIOR APPLICATION NUMBER: 60/091982
;  PRIOR FILING DATE: 1998-07-07
;  PRIOR APPLICATION NUMBER: 60/095302
;  PRIOR FILING DATE: 1998-08-04
;  PRIOR APPLICATION NUMBER: 60/095318
;  PRIOR FILING DATE: 1998-08-04
;  PRIOR APPLICATION NUMBER: 60/095916
;  PRIOR FILING DATE: 1998-08-10
;  PRIOR APPLICATION NUMBER: 60/096146
;  PRIOR FILING DATE: 1998-08-11
;  PRIOR APPLICATION NUMBER: 60/096791
;  PRIOR FILING DATE: 1998-08-17
;  PRIOR APPLICATION NUMBER: 60/097986
;  PRIOR FILING DATE: 1998-08-26
;  PRIOR APPLICATION NUMBER: 60/098544
;  PRIOR FILING DATE: 1998-08-31
;  PRIOR APPLICATION NUMBER: 60/099596
;  PRIOR FILING DATE: 1998-09-09
```

; PRIOR APPLICATION NUMBER: 60/099598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/099803
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099811
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100038
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; PRIOR APPLICATION NUMBER: 60/100385
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; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 98.8%; Score 1048; DB 14; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
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Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
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Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
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Db        183 HLGVQVWQRAECPQVPKI 200
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RESULT 15
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; Publication No. US20030073817A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C78
; CURRENT APPLICATION NUMBER: US/10/227,883
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
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; PRIOR APPLICATION NUMBER: 60/169835

Query Match 98.8%; Score 1048; DB 14; Length 667;
Best Local Similarity 99.0%; Pred. No. 7.3e-95;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
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Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
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Db        123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy        182 HLGVQVWQRAECPQVPKI 199
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Db        183 HLGVQVWQRAECPQVPKI 200
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Search completed: February 8, 2005, 13:45:12
Job time : 67.4599 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 13:29:35 ; Search time 19.3683 Seconds
(without alignments)
988.580 Million cell updates/sec

Title: US-09-816-653A-2
Perfect score: 1061
Sequence: 1 MSQPAGNQTSPGATEDYSYG.....WAHLGVQVWQRAECPQVPKI 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	86.5	8.2	757	2	F87304	beta-N-acetylhexos
2	85.5	8.1	380	2	S35785	glycoprotein I - b
3	84.5	8.0	335	2	T36304	probable anthranil
4	84	7.9	913	2	A48280	receptor tyrosine
5	83	7.8	1172	2	T36053	probable ABC-type
6	80.5	7.6	385	2	E83506	probable MFS trans
7	80	7.5	433	1	VHVUPH	nucleocapsid prote
8	80	7.5	876	2	A49508	protein-tyrosine k
9	80	7.5	921	2	G02326	transcription fact
10	79.5	7.5	249	1	S47153	type IV prepilin p
11	79.5	7.5	577	2	S77715	cytochrome c-type
12	79	7.4	463	2	C47301	virB6 homolog - Bo
13	79	7.4	910	2	A53137	tyrosine kinase re
14	78.5	7.4	477	2	H83588	probable MFS trans
15	78.5	7.4	532	2	JC5412	epidermal growth f
16	78.5	7.4	3519	2	S43048	polyketide synthas
17	78	7.4	419	2	JQ2254	farnesyl-diphospha
18	77.5	7.3	579	2	S35237	cytochrome c-type
19	77	7.3	521	2	AF3287	thiamine transport
20	76.5	7.2	221	2	B48266	protein-tyrosine k
21	76	7.2	394	2	A55045	probable 3-hydroxy
22	76	7.2	666	2	F83340	hypothetical prote
23	76	7.2	709	2	F75584	hypothetical prote
24	75.5	7.1	400	2	T35334	probable membrane
25	75.5	7.1	454	2	T10525	cyclin B1b-11 - ye
26	75.5	7.1	655	1	A42420	L-iduronidase (EC
27	75	7.1	211	2	T09498	cytochrome c bioge
28	75	7.1	230	2	S72714	Lepb1170_F2_64 pro
29	75	7.1	668	2	T01685	crp1 protein - mai
30	74.5	7.0	425	2	C87619	hypothetical prote
31	74	7.0	320	2	A82449	conserved hypothet
32	73.5	6.9	233	2	T47136	hypothetical prote
33	73.5	6.9	300	2	D83487	hypothetical prote
34	73.5	6.9	636	2	JW0047	class I cytokinase
35	73.5	6.9	1174	2	AH0663	probable pyruvate-
36	73.5	6.9	1201	2	A83007	hypothetical prote
37	73	6.9	411	2	D72588	hypothetical prote
38	73	6.9	473	2	T03611	cyclin, B-type - c
39	73	6.9	633	2	F84564	probable protein k
40	73	6.9	739	2	A83015	primosomal protein
41	73	6.9	786	2	F70735	hypothetical prote
42	72.5	6.8	176	2	B83199	hypothetical prote
43	72.5	6.8	258	2	S75950	hypothetical prote
44	72.5	6.8	529	2	C70545	hypothetical prote
45	72.5	6.8	636	1	VCVWFS	env polyprotein -

ALIGNMENTS

RESULT 1
F87304
beta-N-acetylhexosaminidase, probable [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87304
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolo n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: F87304
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-757 <STO>
A;Cross-references: UNIPROT:Q9AAZ5; GB:AE005673; NID:g13421618; PIDN:AAK22434.1; GSPDB:
C;Genetics:
A;Gene: CC0447

Query Match 8.2%; Score 86.5; DB 2; Length 757;
Best Local Similarity 30.6%; Pred. No. 3.7;
Matches 49; Conservative 16; Mismatches 60; Indels 35; Gaps 9;

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Qy         62 VLLLLAMLVRR-RQLWPDCVRGRPGLPSPVDFLAGDRP----------------RAVPA 103
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Qy        104 AVFMVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYY----P 159
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Db        123 GLFYGAMSLWQLATPDEAKGPVALLAASIE-----DAPRFAWR--GLMVDSARHYQSLDT 175

Qy        160 LAACATAGHTAAHLLGSTLSWAHLGVQVWQRAECPQVPKI 199
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Db        176 LKAVIDA--MAAHKL-NTFHWHLVDDQGW-RLEIKKYPKL 211
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RESULT 2
S35785
glycoprotein I - bovine herpesvirus 1
C;Species: bovine herpesvirus 1
C;Date: 09-Jun-1994 #sequence_revision 12-May-1995 #text_change 09-Jul-2004
C;Accession: S35785
R;Audonnet, J.
submitted to the EMBL Data Library, June 1993
A;Reference number: S35782
A;Accession: S35785
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-380 <AUD>
A;Cross-references: UNIPROT:Q08102; EMBL:Z23068; NID:g312185; PIDN:CAA80605.1; PID:g312
C;Superfamily: pseudorabies virus glycoprotein gp63

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C;Keywords: glycoprotein

  Query Match             8.1%;  Score 85.5;  DB 2;  Length 380;
  Best Local Similarity   27.6%;  Pred. No. 2.2;
  Matches   37;  Conservative   12;  Mismatches   38;  Indels   47;  Gaps    6;

Qy          4 PAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLAS----LS 59
              |||   || |:   :: :             || |: |:         :   |||    |
Db        256 PAGPTASPAASPSRAFSA-----AAPAAAAQPAGDTPA--------RFRRQLASILVPLC 302

Qy         60 ILVLLLLAM-------LVRRRQL----------------------WPDCVRGRPGLPSPV 90
              :|||||||:        :||| |                      | |    |  |: |
Db        303 VLVLLLLALCAATVNCALRRRLLPCSRRVYKPRTCAACGSGTCAGRPPCRGAAPSAPATV 362

Qy         91 DFLAGDRPRAVPAA 104
                | | ||:| | |
Db        363 VAL-GSRPKAPPLA 375


RESULT 3
T36304
probable anthranilate phosphoribotransferase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36304
R;Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, March 1999
A;Reference number: Z21604
A;Accession: T36304
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-335 <SAU>
A;Cross-references: UNIPROT:Q9Z4W9; EMBL:AL035654; PIDN:CAB38583.1; GSPDB:GN00070; SCOED
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: trpD2; SCOEDB:SCE8.05c
C;Superfamily: anthranilate phosphoribosyltransferase; trpD homology

  Query Match             8.0%;  Score 84.5;  DB 2;  Length 335;
  Best Local Similarity   30.8%;  Pred. No. 2.4;
  Matches   36;  Conservative   10;  Mismatches   42;  Indels   29;  Gaps    5;

Qy         81 RGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEA 140
              | |||     |   ||  ||| |||   :|:                        |::|
Db        247 RSRPG-----DLAGGD--RAVNAAVLRRVLAG----------------GRGPARDVVLLN 283

Qy        141 PRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWAHLGVQVWQRAECPQVP 197
                | :: |:    :  ` ||| |  |  || ||     |||     ||||:  :||
Db        284 AAAALRVAGVAGTWSDGLRLAASAVDGGAAAGLLD---RWAHAS---WQRADLVEVP 334


RESULT 4
A48280
receptor tyrosine kinase - human
C;Species: Homo sapiens (man)
C;Date: 31-May-1996 #sequence_revision 31-May-1996 #text_change 09-Jul-2004
C;Accession: A48280
R;Johnson, J.D.; Edman, J.C.; Rutter, W.J.
Proc. Natl. Acad. Sci. U.S.A. 90, 5677-5681, 1993
A;Title: A receptor tyrosine kinase found in breast carcinoma cells has an extracellular
A;Reference number: A48280; MUID:93296201; PMID:8390675
A;Accession: A48280
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-913 <RES>
A;Cross-references: UNIPROT:Q08345; GB:L11315; NID:g403386; PIDN:AAA02866.1; PID:g403387
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-ter
C;Keywords: ATP
F;30-185/Domain: discoidin I amino-terminal homology <DN1>
F;608-912/Domain: protein kinase homology <KIN>
F;616-624/Region: protein kinase ATP-binding motif

  Query Match             7.9%;  Score 84;  DB 2;  Length 913;
  Best Local Similarity   22.7%;  Pred. No. 7.7;
  Matches   39;  Conservative   20;  Mismatches   73;  Indels   40;  Gaps    7;

Qy          7 NQTSPGATEDYSYGSWYIDEPQ----GGXELQPEGEVPSCHT-SIPPGLYHACLASLSIL 61
              | :||      :    |:   |        ||:| |: |       |  :   || :: :|
Db        370 NNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILIGCLVAIILL 429

Qy         62 VLLLLAMLV-----------RRRQLWPD-----------CVRGRPGLPSPVDFL---- 93
              :||::|:::             || |  :             :  |||   |  :
Db        430 LLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREPPPYQEPRP 489

Qy         94 AGDRPRAVPAAVFMVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAW 145
              |: | : |     |   |  ||      |   | | |  |   |   | ||
Db        490 RGNPPHSAPC----VPNGSALLLSNPAYRLLLATYARPPRGPG---PPTPAW 534


RESULT 5
T36053
probable ABC-type transport protein cydCD - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T36053
R;Saunders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.
submitted to the EMBL Data Library, November 1998
A;Reference number: Z21595
A;Accession: T36053
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-1172 <SAU>
A;Cross-references: UNIPROT:Q9ZBY5; EMBL:AL034355; PIDN:CAA22219.1; GSPDB:GN00070; SCOEI
A;Experimental source: strain A3(2)
C;Genetics:
A;Gene: cydCD; SCOEDB:SCD78.14
C;Superfamily: Mycobacterium tuberculosis probable ABC transporter Rv0194; ATP-binding c

  Query Match             7.8%;  Score 83;  DB 2;  Length 1172;
  Best Local Similarity   31.5%;  Pred. No. 12;
  Matches   45;  Conservative   12;  Mismatches   68;  Indels   18;  Gaps    5;

Qy         55 LASLSILVLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLC 114
              ||:   :: | ||:  |:| :      |    | :|       : ||  ||  | |::  |
Db        874 LAAFEAVLGLPLAVQYRQR-VRRSAERVYEVLDAPEPVREPEVPRQAPATPFPVVVEGLA 932

Qy        115 LLLP--DEDALPFLTL---------ASAPSQDGKTEAPRGAWKILGLFHYAALYYPLA-- 161
                 |  | |||  | |           ||  |||     |  :|     ||  | ||
Db        933 ARHPGQDRDALAGLDLTLEQGRRVAVVGPSGSGKTTL---AQVLLRFLDSAAGSYTLAGV 989

Qy        162 -ACATAGHTAAHLLGSTLSWAHL 183
                | | ||      |:|     |||
Db        990 DAYALAGDDVRRLVGLCAQDAHL 1012


RESULT 6
E83506
probable MFS transporter PA1108 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: E83506
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: E83506
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-385 <STO>
A;Cross-references: UNIPROT:Q9I4M7; GB:AE004541; GB:AE004091; NID:g9947024; PIDN:AAG0449
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA1108
```

```
  Query Match             7.6%;  Score 80.5;  DB 2;  Length 385;
  Best Local Similarity   29.0%;  Pred. No. 6.6;
  Matches   54;  Conservative   14;  Mismatches   57;  Indels   61;  Gaps   13;

Qy         27 PQGGXELQPEGEVPSCHTSIPPGLYHACLASLSILVLLLLAMLVRRRQLWPDCVRGRP-- 84
              | ||  |   |  |             |  |:|::|:  | |::|     ||:    ||
Db        148 PLGGQWLADLGGHP-----------AVFATLAVLLASLAALVV---PAWPET---RPLL 189

Qy         85 -GLPSPVDF-----LAGDRP---RAVPAAVFMVLLSSLC----LLLPDEDALPF----LT 127
               | | |          :  |||   ||:  ||  ||: |       :: |   | |    |
Db        190 AGTPEPATLAIFRRVLADRPLQTRALLVAVLNVLVFSFYAAGPFMVGDLPGLGFGWIGLA 249

Qy        128 LASAPSQDG--KTEAPRGAWKI-----LGLFHYAALYYPLAACATAGHTAAHLLGST--- 177
              :| | |          ||  |       |||           | | || ||  || :
Db        250 IAIAGSLGALLNRRLPR-TWNSARRVRLGL----------ALAAAGATAQTLLAAVGYA 297

Qy        178 --LSWA 181
                | ||
Db        298 EGLYWA 303


RESULT 7
VHVUPH
nucleocapsid protein N - Prospect Hill virus (strain PHV-1)
N;Alternate names: nucleoprotein N
C;Species: Prospect Hill virus
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: A34681
R;Parrington, M.A.; Kang, C.Y.
Virology 175, 167-175, 1990
A;Title: Nucleotide sequence analysis of the S genomic segment of Prospect Hill virus: c
A;Reference number: A34681; MUID:90177212; PMID:2309440
A;Accession: A34681
A;Molecule type: genomic RNA
A;Residues: 1-433 <PAR>
A;Cross-references: UNIPROT:P22047
C;Genetics:
A;Gene: N
A;Map position: segment S
C;Superfamily: Hantaan virus nucleocapsid protein
C;Keywords: nucleocapsid; nucleoprotein

  Query Match             7.5%;  Score 80;  DB 1;  Length 433;
  Best Local Similarity   24.1%;  Pred. No. 8.4;
  Matches   35;  Conservative   21;  Mismatches   55;  Indels   34;  Gaps    6;

Qy         23 YIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSILVLLL----LAMLVRRRQLWPD 78
              |:  |     :: |   |    :|  ||: | : : :|:  ::     |  |:    | |
Db        178 YVSMPTAQSTMKAEELTPGRFRTIVCGLFPAQIMARNIISPVMGVIGFAFFVKD---WAD 234

Qy         79 CVRG------------RPGLPS-PVDFLAGDRPRAVPAAVFMVLLSSLCLL----LPDE 120
               |:              ||| |:   :||:  |           |::   :|    |||
Db        235 KVKAFLDQKCPFLKAEPRPGQPAGEAEFLSSIR---------AYLMNRQAVLDETHLPDI 285

Qy        121 DALPFLTLASAPSQDGKTEAPRGAW 145
              |||  |  :  |:     | |  ||
Db        286 DALVELAASGDPTLPDSLENPHAAW 310


RESULT 8
A49508
protein-tyrosine kinase (EC 2.7.1.112) trkE precursor - human
C;Species: Homo sapiens (man)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: A49508; I38358; S37402
R;Di Marco, E.; Cutuli, N.; Guerra, L.; Cancedda, R.; De Luca, M.
J. Biol. Chem. 268, 24290-24295, 1993
A;Title: Molecular cloning of trkE, a novel trk-related putative tyrosine kinase recepto
A;Reference number: A49508; MUID:94043265; PMID:8226977
A;Accession: A49508
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-876 <DIA>
A;Cross-references: UNIPROT:Q08345; EMBL:X74979; NID:g400462; PIDN:CAA52915.1; PID:g4004
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-ter
C;Keywords: ATP; phosphotransferase; tyrosine-specific protein kinase
F;30-185/Domain: discoidin I amino-terminal homology <DN1>
F;571-875/Domain: protein kinase homology <KIN>
F;579-587/Region: protein kinase ATP-binding motif

  Query Match             7.5%;  Score 80;  DB 2;  Length 876;
  Best Local Similarity   20.6%;  Pred. No. 17;
  Matches   42;  Conservative   26;  Mismatches   74;  Indels   62;  Gaps    9;

Qy          7 NQTSPGATEDYSYGSWYIDEPQ----GGXELQPEGEVPSCHT-SIPPGLYHACLASLSIL 61
              | :||     :    |:   |        ||:| |: |       |  :   || :: :|
Db        370 NNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILIGCLVAIILL 429

Qy         62 VLLLLAMLV-----------RRRQLWPD-----------CVRGRPGLPSPVDFLAGDR 97
              :||::|:::             || |  :             :  |||   |  :    |
Db        430 LLLIIALMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREPPPY-QEPR 488

Qy         98 PRAVPAAVFMVLLSSLCL----------LLPDEDALPFLTLASAPSQDGKTEAPRGAWKI 147
              ||  |        |: |:          : |::   | |     | |:
Db        489 PRGNPPH------SAPCVPNGSAYSGDYMEPEKPGAPLL---PPPPQN----------- 527

Qy        148 LGLFHYAALYYPLAACATAGHTAA 171
                : |||           | |:| |
Db        528 -SVPHYAEADIVTLQGVTGGNTYA 550


RESULT 9
G02326
transcription factor NFAT1 isoform B - human
C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: G02326
R;Luo, C.
submitted to the EMBL Data Library, December 1995
A;Reference number: H01056
A;Accession: G02326
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-921 <LUO>
A;Cross-references: UNIPROT:Q13469; EMBL:U43341; NID:g1353773; PIDN:AAC50886.1; PID:g13
C;Genetics:
A;Gene: NFAT1

  Query Match             7.5%;  Score 80;  DB 2;  Length 921;
  Best Local Similarity   23.5%;  Pred. No. 18;
  Matches   57;  Conservative   30;  Mismatches   76;  Indels   80;  Gaps   15;

Qy          3 QPAGNQTSPGATEDYSYGSWYIDEPQGGX-------ELQPEGEV-PSCHTSIPPGLYHAC 54
              :||   :||||   :|     :  | |            ||   | |  | | | | |  :
Db        240 RPASRSSSPGAKRRHSCAEALVALPPGASPQRSRSPSPQPSSHVAPQDHGS-PAG--YPP 296

Qy         55 LASLSILVLLLLAMLVRR-----RQLW-----PDCVRGRP---GLP----SPVDFLA--- 94
              :|  ::::  | ::           ::|     |  |   |  |||      |:||
Db        297 VAGSAVIMDALNSLATDSPCGIPPKMWKTSPDPSPVSAAPSKAGLPRHIYPAVEFLGPCE 356

Qy         95 -GDRPRAVPAAVFMVLLSSLCLLLPDEDALPFLTL---ASAP-------SQDG------- 136
               |:|  : | :: :|  :    |:|   |:|  ::   || |       || |
Db        357 QGERRNSAPESILLVPPTWPKPLVP---AIPICSIPVTASLPPLEWPLSSQSGSYELRIE 413

Qy        137 -----------KTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWAHLGV 185
                        :||  ||| |                 | ||    | |  :    ||:
Db        414 VQPKPHHRAHYETEGSRGAVK---------------APTGGHPVVQLHG-YMENKPLGL 456

Qy        186 QVW 188
               |::
Db        457 QIF 459


RESULT 10
S47153
type IV prepilin peptidase (EC 3.4.99.-) BfpP - Escherichia coli
```

```
N;Contains: type IV pilin N-methyltransferase (EC 2.1.1.-)
C;Species: Escherichia coli
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C;Accession: S47153; S70974
R;Zhang, H.; Lory, S.; Donnenberg, M.S.
submitted to the EMBL Data Library, June 1994
A;Description: A plasmid encoded prepilin peptidase from enteropathogenic Escherichia co
A;Reference number: S47153
A;Accession: S47153
A;Molecule type: DNA
A;Residues: 1-249 <ZHA>
A;Cross-references: UNIPROT:Q57382; EMBL:Z34464; NID:g499386; PIDN:CAA84229.1; PID:g4993
R;Stone, K.D.; Zhang, H.Z.; Carlson, L.K.; Donnenberg, M.S.
Mol. Microbiol. 20, 325-337, 1996
A;Title: A cluster of fourteen genes from enteropathogenic Escherichia coli is sufficien
A;Reference number: S70966; MUID:96310370; PMID:8733231
A;Accession: S70974
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-249 <STO>
A;Cross-references: EMBL:Z68186; NID:g1122399; PIDN:CAA92334.1; PID:g1122408
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1995
C;Genetics:
A;Gene: bfpP
C;Superfamily: type IV prepilin peptidase
C;Keywords: hydrolase; methyltransferase; S-adenosylmethionine

  Query Match             7.5%;  Score 79.5;  DB 1;  Length 249;
  Best Local Similarity   25.8%;  Pred. No. 5.2;
  Matches   41;  Conservative   11;  Mismatches   62;  Indels   45;  Gaps    6;

Qy         22 WYIDEPQGGXELQPEGEVPSCHTSIP----------------------PGLYHACLASLS 59
              ||   | | |    ||   ||  :|                      || | : ||
Db         60 WYYLIPVLGYFL-CRGECGYCHAKVPVRYPLTEFICGVCSVIIFVFLGDRLYDAVIVSLL 118

Qy         60 ILVLLLLAMLVRRRQLWPDCVRG--------RPGLPSPVDFLAGDRPRAVPAAVFMVLLS 111
               | |: ||::  |    | ||           ||  |  | : |    |    : | :
Db        119 FLCLVFLALIDLRENWLPACVTYPLFWAGMITPGFASSDDKIFG----AFTGFLIMYISM 174

Qy        112 SLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAWKILGL 150
              |   | ||      :| | :         |||  ||:
Db        175 KLVSALRKEDVFAGGDIALATA--------AGAW--LGI 203


RESULT 11
S77715
cytochrome c-type biogenesis protein homolog - evening primrose mitochondrion
C;Species: mitochondrion Oenothera villaricae (evening primrose)
C;Date: 06-Sep-1996 #sequence_revision 09-May-1997 #text_change 24-Sep-1999
C;Accession: S77715; S35238; S77730
R;Schuster, W.; Combettes, B.; Flieger, K.; Brennicke, A.
Mol. Gen. Genet. 239, 49-57, 1993
A;Title: A plant mitochondrial gene encodes a protein involved in cytochrome c biogenesi
A;Reference number: S35237; MUID:93288005; PMID:8389979
A;Accession: S77715
A;Molecule type: mRNA
A;Residues: 1-577 <SCH>
A;Cross-references: EMBL:X69555
A;Note: the source is designated as Oenothera berteriana
A;Note: 10-Ser, 13-Leu, 33-Leu, 46-Leu, 48-Cys, 51-Ser, 86-Trp, 88-Leu, 106-Val, 112-Tyr
-Cys, 259-Leu, 263-Leu, 268-Leu, 306-Trp, 325-Phe, 368-Leu, 424-Trp, 433-Leu, 439-Tyr, 4
A;Note: this represents all RNA editing sites; individual clones show partial RNA editin
A;Accession: S35238
A;Molecule type: DNA
A;Residues: 1-9,'P',11-12,'P',14-32,'P',34-45,'S',47,'R',49-50,'P',52-85,'R',87,'P',89-1
,'P',237-238,'S',240-243,'P',245-246,'R',248-251,'R',253-258,'S',260-262,'P',264-267,'S'
2-466,'R',468-480,'S',482-487,'L',489-577 <SCF>
A;Cross-references: EMBL:X69555
R;Schuster, W.
submitted to the EMBL Data Library, February 1992
A;Reference number: S77730
A;Accession: S77730
A;Molecule type: DNA
A;Residues: 1-9,'P',11-12,'P',14-32,'P',34-45,'S',47,'R',49-50,'P',52-85,'R',87,'P',89-1
,'P',237-238,'S',240-243,'P',245-246,'R',248-251,'R',253-258,'S',260-262,'P',264-267,'S'
2-466,'R',468-480,'S',482-487,'L',489-577 <SCW>
A;Cross-references: EMBL:X69555; NID:g14026; PIDN:CAA49287.1; PID:g14027
C;Genetics:
A;Genome: mitochondrion
C;Superfamily: mitochondrial cycK-related protein
C;Keywords: mitochondrion; RNA editing

  Query Match             7.5%;  Score 79.5;  DB 2;  Length 577;
  Best Local Similarity   22.9%;  Pred. No. 13;
  Matches   25;  Conservative   18;  Mismatches   49;  Indels   17;  Gaps    2;

Qy         13 ATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSILVLLLLAMLVRR 72
              |  :  :| |:  :|  -      |      :|  |:   | |:|   ::|:  |
Db        438 AYHELGWGGWWFWDPVENASFMPWVLATACIHSVILPLLHSCTLLINIVTFLC------- 490

Qy         73 RQLWPDCVRG----RPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLL 117
                 || |    | || : |   | |  | :    | :|:: : ::|
Db        491 ------CVLGTFSIRSGLLASVHSFATDDTRGIFLWRFFLLMTGISMIL 533


RESULT 12
C47301
virB6 homolog - Bordetella pertussis
C;Species: Bordetella pertussis
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 20-Sep-1999
C;Accession: C47301
R;Weiss, A.A.; Johnson, F.D.; Burns, D.L.
Proc. Natl. Acad. Sci. U.S.A. 90, 2970-2974, 1993
A;Title: Molecular characterization of an operon required for pertussis toxin secretion.
A;Reference number: A47301; MUID:93219406; PMID:8464913
A;Contents: BP338
A;Accession: C47301
A;Status: preliminary
A;Molecule type: nucleic acid
A;Residues: 1-463 <WEI>
A;Note: sequence extracted from NCBI backbone (NCBIN:128775, NCBIP:128778)
C;Superfamily: Bordetella pertussis virB6 homolog

  Query Match             7.4%;  Score 79;  DB 2;  Length 463;
  Best Local Similarity   26.3%;  Pred. No. 11;
  Matches   54;  Conservative   18;  Mismatches   71;  Indels   62;  Gaps   11;

Qy          5 AGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTS---IPPGLYHACLASLS-- 59
              | |  :||:  ::   :  :    ||           |  :   | |||    | ||
Db        220 AANDANPGSAVNWLLCAMIVAASAGGW---------LCLAASLLIVPGLIVTLLLSLGPL 270

Qy         60 ILVLLLLAMLVRRRQLWPDCV--------RGRPGLPSPVDFLAGDRPRAVPAAV------ 105
               |||||   | |    |   :         | | :    | |||  |  :|
Db        271 FLVLLLFPALQRWTNAWLGALVRALVFMALGTPAVGLLSDVLAGALPAGLPQRFATDPLR 330

Qy        106 FMVLLSSLC----LLLPDEDALPFLTLASA-----------PSQDGKTEAPRGAWKILG 149
              :| ::||    |:|     |  : |||:            :  |  :| | |
Db        331 STMLAATLCATATLML-----LTLVPLASSVNAGLRRRLWPNAAHPGLAQAHRQA----- 380

Qy        150 LFHYAALYY---PLAACATAG-HTA 170
                ||  |   | || | || | |
Db        381 ----AARQYAPRPAAAAAAAGPHQA 401


RESULT 13
A53137
tyrosine kinase receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: A53137
R;Sanchez, M.P.; Tapley, P.; Saini, S.S.; He, B.; Pulido, D.; Barbacid, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 1819-1823, 1994
A;Title: Multiple tyrosine protein kinases in rat hippocampal neurons: isolation of Ptk-
A;Reference number: A53137; MUID:94173920; PMID:8127887
A;Accession: A53137
A;Status: preliminary; translated from GB/EMBL/DDBJ
```

```
A;Molecule type: DNA
A;Residues: 1-910 <RES>
A;Cross-references: UNIPROT:Q63474; GB:L26525; NID:g432480; PIDN:AAA21089.1; PID:g432481
C;Genetics:
A;Gene: Ptk-3
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; discoidin I amino-ter
C;Keywords: ATP
F;31-186/Domain: discoidin I amino-terminal homology <DN1>
F;605-909/Domain: protein kinase homology <KIN>
F;613-621/Region: protein kinase ATP-binding motif

  Query Match             7.4%;  Score 79;  DB 2;  Length 910;
  Best Local Similarity   22.1%;  Pred. No. 22;
  Matches   36;  Conservative   23;  Mismatches   70;  Indels   34;  Gaps    7;

Qy         13 ATEDYSYGSWYIDEPQ----GGXELQPEGEVPSCHT-SIPPGLYHACLASLSILVLLLLA 67
              ::: :    |:   |        ||:| |: |       |  :   || :: :|:||::|
Db        373 SSDTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILIGCLVAIILLLLLIIA 432

Qy         68 MLV-----------RRRQLWPD-----------CVRGRPGLPSPVDFLAGDRPRAVPA 103
              :::              || |  :           :  |||   |  :    |||  |
Db        433 LMLWRLHWRRLLSKAERRVLEEELTVHLSVPGDTILINNRPGPREPPPY-QEPRPRGTPT 491

Qy        104 AVFMVLLSSLCLLLPDED-ALPFLTLASAPSQDGKTEAPRGAW 145
                : :   ||| :    |   | | |   |    |  ||
Db        492 HSAPCVPNGSALLLSNPAYRLLLATYARPPRGPG---PPTPAW 531


RESULT 14
H83588
probable MFS transporter PA0458 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83588
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83588
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-477 <STO>
A;Cross-references: UNIPROT:Q9I660; GB:AE004483; GB:AE004091; NID:g9946313; PIDN:AAG0384
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA0458
C;Superfamily: multidrug-efflux transporter

  Query Match             7.4%;  Score 78.5;  DB 2;  Length 477;
  Best Local Similarity   26.5%;  Pred. No. 13;
  Matches   54;  Conservative   16;  Mismatches   63;  Indels   71;  Gaps   11;

Qy         19 YGSWY----IDEPQG------GXELQPE--GEVPSCHTSIPPGLYHACLASLSI------ 60
              | ||:    |: | |        :| |:    |||   ||  |:   :  :||
Db        164 YASWHWIFLINLPVGLLGCLVAMKLMPDLRSPVPSRFDSIGFLLFGGSMVLISIALEGLG 223

Qy         61 --------LVLLLLAMLVRRRQLWPDCVR-GRPGLPSPVDFLAGDRPRAVPAAVFMV-LL 110
                    :||||:  ||      |   :|  :|  |           |     |  | | :|
Db        224 ELHLSHLRVVLLLIGGLVLLTAYWLRALRIDKPLFP----------PSLFKARTFAVGIL 273

Qy        111 SSLCLLLPDEDALPFLT-------LASAPSQDGKTEAPRG---------AWKILGLFHYA 154
               :|   |    ||||||        |   ||  | |  |           |  :|  | |
Db        274 GNLFARL-GSGALPFLTPLLLQVGLGYPPSTAGMTMIPLALFAMVAKPMAKPLLDFFGYR 332

Qy        155 ALYYPLAACATAGHTAAHLLGSTL 178
               |               |:|:||
Db        333 KL---------------LVGNTL 340


RESULT 15
JC5412
epidermal growth factor receptor-binding protein GRB-7 - human
C;Species: Homo sapiens (man)
C;Date: 10-Jun-1997 #sequence_revision 18-Jul-1997 #text_change 09-Jul-2004
C;Accession: JC5412
R;Kishi, T.; Sasaki, H.; Akiyama, N.; Ishizuka, T.; Sakamoto, H.; Aizawa, S.; Sugimura,
Biochem. Biophys. Res. Commun. 232, 5-9, 1997
A;Title: Molecular cloning of human GRB-7 co-amplified with CAB1 and c-ERBB-2 in primary
A;Reference number: JC5412; MUID:97236270; PMID:9125150
A;Accession: JC5412
A;Molecule type: mRNA
A;Residues: 1-532 <KIS>
A;Cross-references: UNIPROT:Q14451; DDBJ:D43772; NID:g601890; PIDN:BAA07827.1; PID:g601
C;Comment: This protein contains a pleckstrin domain which mediates protein-protein int
C;Genetics:
A;Gene: GDB:GRB7
A;Cross-references: GDB:1297554; OMIM:601522
F;231-336/Domain: pleckstrin #status predicted <PLE>
F;432-532/Domain: SH2 #status predicted <SH2>

  Query Match             7.4%;  Score 78.5;  DB 2;  Length 532;
  Best Local Similarity   28.3%;  Pred. No. 14;
  Matches   39;  Conservative   12;  Mismatches   62;  Indels   25;  Gaps    7;

Qy         75 LWPDCVRGRPGLPSPVDF-LAGDRPRAVPAAVFMVLLSSLCLLLPDEDAL---------P 124
              |||       || | | |  |  :  |: |     :|: :    | :|:           |
Db         17 LWP-APGTPPGTPRPPDTPLPEEVKRSQP-----LLIPTTGRKLREEERRATSLPSIPNP 70

Qy        125 FLTLASAPSQDGKTEAPRGAWKIL----GLFHYAALYYPLAAC----ATAGHTAAHLLGS 176
              |  | | |||       |  |  :|       |   :|    ||      || || |:
Db         71 FPELCSPPSQSPILGGPSSARGLLPRDASRPHVVKVYSEDGACRSVEVAAGATARHVCEM 130

Qy        177 TLSWAH-LGVQVWQRAEC 193
               :  || |  : |   ||
Db        131 LVQRAHALSDETWGLVEC 148


Search completed: February  8, 2005, 13:41:04
Job time : 21.8683 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 13:21:20 ; Search time 87.3473 Seconds
(without alignments)
1166.650 Million cell updates/sec

Title: US-09-816-653A-2
Perfect score: 1061
Sequence: 1 MSQPAGNQTSPGATEDYSYG.....WAHLGVQVWQRAECPQVPKI 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1048	98.8	667	2	Q8TB21	Q8tb21 homo sapien
2	1048	98.8	667	2	Q9BX79	Q9bx79 homo sapien
3	1048	98.8	708	2	Q7Z3U9	Q7z3u9 homo sapien
4	986.5	93.0	658	2	Q9BX78	Q9bx78 homo sapien
5	745	70.2	159	2	Q6PJF8	Q6pjf8 homo sapien
6	697	65.7	670	2	O70491	O70491 mus musculu
7	697	65.7	670	2	Q6DIA8	Q6dia8 mus musculu
8	488	46.0	560	2	Q7L9G1	Q7l9g1 homo sapien
9	427	40.2	137	2	Q8C442	Q8c442 mus musculu
10	337	31.8	238	2	Q6DGZ6	Q6dgz6 brachydanio
11	99.5	9.4	293	2	Q7WE26	Q7we26 bordetella
12	96.5	9.1	293	2	Q7W325	Q7w325 bordetella
13	96.5	9.1	441	2	Q6ZNR9	Q6znr9 homo sapien
14	90.5	8.5	840	2	Q7NIK1	Q7nik1 gloeobacter
15	90.5	8.5	2527	2	Q7W6G2	Q7w6g2 bordetella
16	90	8.5	263	1	Y8K6_ENCCU	Q8sui0 encephalito
17	89.5	8.4	750	2	Q9YQ39	Q9yq39 suid herpes
18	88.5	8.3	435	2	Q854B3	Q854b3 mycobacteri
19	87.5	8.2	318	2	Q7NTK1	Q7ntk1 chromobacte
20	87.5	8.2	336	2	Q94LD3	Q94ld3 oryza sativ
21	87.5	8.2	413	2	Q8XRV5	Q8xrv5 ralstonia s
22	87	8.2	848	2	Q84SK5	Q84sk5 oryza sativ
23	86.5	8.2	757	2	Q9AAZ5	Q9aaz5 caulobacter
24	85.5	8.1	380	1	VGLI_BHV1S	Q08102 bovine herp
25	85.5	8.1	569	2	Q8Y1X8	Q8y1x8 ralstonia s
26	85	8.0	398	2	Q73UR0	Q73ur0 mycobacteri
27	84.5	8.0	335	1	TRD2_STRCO	Q9z4w9 streptomyce
28	84.5	8.0	382	2	O39505	O39505 bovine herp
29	84.5	8.0	382	2	Q76PF0	Q76pf0 bovine herp
30	84.5	8.0	730	2	Q93QX7	Q93qx7 corynebacte
31	84.5	8.0	2527	2	Q7WID3	Q7wid3 bordetella
32	84	7.9	295	2	Q6ZJA8	Q6zja8 oryza sativ
33	84	7.9	909	1	DDR1_PANTR	Q7yr43 pan troglod
34	84	7.9	913	1	DDR1_HUMAN	Q08345 h epithelia
35	84	7.9	917	2	Q767M4	Q767m4 sus scrofa
36	83.5	7.9	482	2	Q6Z576	Q6z576 oryza sativ
37	83	7.8	281	1	CEBE_RAT	P56261 rattus norv
38	83	7.8	344	2	Q7WMZ6	Q7wmz6 bordetella
39	83	7.8	496	2	Q72HN1	Q72hn1 thermus the
40	83	7.8	1172	2	Q9ZBY5	Q9zby5 streptomyce
41	82	7.7	208	2	Q36437	Q36437 lasaea sp.
42	82	7.7	281	2	Q6PZD9	Q6pzd9 mus musculu
43	82	7.7	333	2	Q7WBH4	Q7wbh4 bordetella
44	82	7.7	2641	2	Q9BXD4	Q9bxd4 homo sapien
45	81.5	7.7	521	2	Q7NT97	Q7nt97 chromobacte

ALIGNMENTS

RESULT 1
Q8TB21
ID Q8TB21 PRELIMINARY; PRT; 667 AA.
AC Q8TB21;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Stimulated by retinoic acid gene 6.
GN Name=FLJ12541;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC025256; AAH25256.1; -.
SQ SEQUENCE 667 AA; 73532 MW; 120685F4635CB0E5 CRC64;

Query Match 98.8%; Score 1048; DB 2; Length 667;
Best Local Similarity 99.0%; Pred. No. 6.9e-88;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy         122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
                |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db         123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy         182 HLGVQVWQRAECPQVPKI 199
                ||||||||||||||||||
Db         183 HLGVQVWQRAECPQVPKI 200
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RESULT 2
Q9BX79
ID Q9BX79 PRELIMINARY; PRT; 667 AA.
AC Q9BX79; Q9H9U8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE STRA6 isoform 1.
GN ORFNames=UNQ3126;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Szeto W., Jiang W., Tice D.A., Rubinfeld B., Hollingshead P.G.,
RA Fong S.E., Dugger D.L., Pham T., Yansura D.G., Wong T.A.,
RA Grimaldi J.C., Corpuz R.T., Singh J.S., Frantz G.D., Devaux B.,
RA Crowley C.W., Schwall R.H., Eberhard D.A., Rastelli L., Polakis P.,
RA Pennica D.;
RT "Overexpression of the retinoic acid-responsive gene Stra6 in human
RT cancers and its synergistic induction by Wnt-1 and retinoic acid.";
RL Cancer Res. 0:0-0(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AF352728; AAK30289.1; -.
DR EMBL; AY359089; AAQ89447.1; -.
SQ SEQUENCE 667 AA; 73502 MW; D20840A46998BA2E CRC64;

Query Match 98.8%; Score 1048; DB 2; Length 667;
Best Local Similarity 99.0%; Pred. No. 6.9e-88;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy           2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
               |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db           3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy          62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy         122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
               |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db         123 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 182

Qy         182 HLGVQVWQRAECPQVPKI 199
               ||||||||||||||||||
Db         183 HLGVQVWQRAECPQVPKI 200
```

RESULT 3
Q7Z3U9
ID Q7Z3U9 PRELIMINARY; PRT; 708 AA.
AC Q7Z3U9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686P1959 (Fragment).
GN Name=DKFZp686P1959;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human endometrium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BX537413; CAD97655.1; -.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 708 AA; 77825 MW; DB88B84AEAD286ED CRC64;

Query Match 98.8%; Score 1048; DB 2; Length 708;
Best Local Similarity 99.0%; Pred. No. 7.3e-88;
Matches 196; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```
Qy           2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
               |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          44 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 103

Qy          62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         104 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 163

Qy         122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
               |||||||||||||||||||||||||||||:||||||||||||||||||||||||||||||
Db         164 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 223

Qy         182 HLGVQVWQRAECPQVPKI 199
               ||||||||||||||||||
Db         224 HLGVQVWQRAECPQVPKI 241
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RESULT 4
Q9BX78
ID Q9BX78 PRELIMINARY; PRT; 658 AA.
AC Q9BX78;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE STRA6 isoform 2.
GN ORFNames=UNQ3126;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Szeto W., Jiang W., Tice D.A., Rubinfeld B., Hollingshead P.G.,
RA Fong S.E., Dugger D.L., Pham T., Yansura D.G., Wong T.A.,
RA Grimaldi J.C., Corpuz R.T., Singh J.S., Frantz G.D., Devaux B.,
RA Crowley C.W., Schwall R.H., Eberhard D.A., Rastelli L., Polakis P.,
RA Pennica D.;
RT "Overexpression of the retinoic acid-responsive gene Stra6 in human
RT cancers and its synergistic induction by Wnt-1 and retinoic acid.";
RL Cancer Res. 0:0-0(2001).
RN [2]
RP SEQUENCE FROM N.A.

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RX   MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA   Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA   Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA   Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA   Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA   Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA   Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA   Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA   Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA   Godowski P.;
RT   "The secreted protein discovery initiative (SPDI), a large-scale
RT   effort to identify novel human secreted and transmembrane proteins: a
RT   bioinformatics assessment.";
RL   Genome Res. 13:2265-2270(2003).
DR   EMBL; AF352729; AAK30290.1; -.
DR   EMBL; AY358748; AAQ89108.1; -.
SQ   SEQUENCE   658 AA;  72582 MW;  5405281727F647DD CRC64;

  Query Match             93.0%;  Score 986.5;  DB 2;  Length 658;
  Best Local Similarity   94.4%;  Pred. No. 3.1e-82;
  Matches  187;  Conservative    1;  Mismatches    1;  Indels    9;  Gaps    1;

Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              |||||||||||||||||||||||||         |||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLP---------RPRAVPAAVFMVLLSSLCLLLPDED 113

Qy        122 ALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWA 181
              |||||||||||||||||||||||||||||:|||||||||||||||||||||||||||||||
Db        114 ALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATAGHTAAHLLGSTLSWA 173

Qy        182 HLGVQVWQRAECPQVPKI 199
              ||||||||||||||||||
Db        174 HLGVQVWQRAECPQVPKI 191


RESULT 5
Q6PJF8
ID   Q6PJF8       PRELIMINARY;       PRT;   159 AA.
AC   Q6PJF8;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   FLJ12541 protein.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Muscle;
RA   Strausberg R.;
RL   Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC015881; AAH15881.1; -.
SQ   SEQUENCE   159 AA;  17190 MW;  7FB62BED986EC3B9 CRC64;

  Query Match             70.2%;  Score 745;  DB 2;  Length 159;
  Best Local Similarity   99.3%;  Pred. No. 1.2e-60;
  Matches  141;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          2 SQPAGNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSIL 61
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db          3 SQPAGNQTSPGATEDYSYGSWYIDEPQGGEELQPEGEVPSCHTSIPPGLYHACLASLSIL 62

Qy         62 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         63 VLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDED 122

Qy        122 ALPFLTLASAPSQDGKTEAPRG 143
              |||||||||||||||||||||
Db        123 ALPFLTLASAPSQDGKTEAPRG 144


RESULT 6
O70491
ID   O70491       PRELIMINARY;       PRT;   670 AA.
AC   O70491;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   Retinoic acid-responsive protein.
GN   Name=Stra6;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95377533; PubMed=7649373; DOI=10.1006/dbio.1995.1226;
RA   Bouillet P., Oulad-Abdelghani M., Vicaire S., Garnier J.M.,
RA   Schuhbaur B., Dolle P., Chambon P.;
RT   "Efficient cloning of cDNAs of retinoic acid-responsive genes in P19
RT   embryonal carcinoma cells and characterization of a novel mouse gene,
RT   Stra1 (mouse LERK-2/Eplg2).";
RL   Dev. Biol. 170:420-433(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97346723; PubMed=9203140; DOI=10.1016/S0925-4773(97)00039-7;
RA   Bouillet P., Sapin V., Chazaud C., Messaddeq N., Decimo D., Dolle P.,
RA   Chambon P.;
RT   "Developmental expression pattern of Stra6, a retinoic acid-responsive
RT   gene encoding a new type of membrane protein.";
RL   Mech. Dev. 63:173-186(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Bouillet P.;
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF062476; AAC16016.1; -.
DR   MGD; MGI:107742; Stra6.
DR   GO; GO:0016021; C:integral to membrane; TAS.
SQ   SEQUENCE   670 AA;  73774 MW;  6ACE69F3EE16A4F7 CRC64;

  Query Match             65.7%;  Score 697;  DB 2;  Length 670;
  Best Local Similarity   68.6%;  Pred. No. 1.4e-55;
  Matches  133;  Conservative   18;  Mismatches   41;  Indels    2;  Gaps    1;

Qy          6 GNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSILVLLL 65
              |:||| | |:|||  ||||:|| |  |:|||| :| |  : || | ||||||||| |||||
Db          9 GSQTSSGVTDDYS--SWYIEEPLGAEEVQPEGVIPLCQLTAPPALLHACLASLSFLVLLL 66
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Qy          66 LAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDEDALPF 125
               ||:|||||:||| |     ||||||||||||    ||||||:|| |:|||||||: |||
Db          67 LALLVRRRRLWPRCGHRGLGLPSPVDFLAGDLSWTVPAAVFVVLFSNLCLLLPDENPLPF 126

Qy         126 LTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWAHLGV 185
               | | :| | ||: |  || ||:| | :| ||||||||||:||| || |||: ||||| ||
Db         127 LNLTAASSPDGEMETSRGPWKLLALLYYPALYYPLAACASAGHQAAFLLGTVLSWAHFGV 186

Qy         186 QVWQRAECPQVPKI 199
               ||||:||||| |||
Db         187 QVWQKAECPQDPKI 200
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RESULT 7
Q6DIA8
ID Q6DIA8 PRELIMINARY; PRT; 670 AA.
AC Q6DIA8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Stra6 protein.
GN Name=Stra6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Eye;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Eye;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC075657; AAH75657.1; -.
DR GO; GO:0016021; C:integral to membrane; TAS.
SQ SEQUENCE 670 AA; 73715 MW; 96F963788EF91249 CRC64;

Query Match 65.7%; Score 697; DB 2; Length 670;
Best Local Similarity 68.6%; Pred. No. 1.4e-55;
Matches 133; Conservative 18; Mismatches 41; Indels 2; Gaps 1;

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Qy           6 GNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSILVLLL 65
               |:||| | |:||| ||||:|| |  |:|||| :| |  : || | |||||||| |||||
Db           9 GSQTSSGVTDDYS--SWYIEEPLGAEEVQPEGVIPLCQLTAPPALLHACLASLSFLVLLL 66

Qy          66 LAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDEDALPF 125
               ||:|||||:||| |     ||||||||||||    ||||||:|| |:|||||||: |||
Db          67 LALLVRRRRLWPRCGHRGLGLPSPVDFLAGDLSWTVPAAVFVVLFSNLCLLLPDENPLPF 126

Qy         126 LTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWAHLGV 185
               | | :| | ||: |  || ||:| | :| ||||||||||:||| || |||: ||||| ||
Db         127 LNLTAASSPDGEMETSRGPWKLLALLYYPALYYPLAACASAGHQAAFLLGTVLSWAHFGV 186

Qy         186 QVWQRAECPQVPKI 199
               ||||:||||| |||
Db         187 QVWQKAECPQDPKI 200
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RESULT 8
Q7L9G1
ID Q7L9G1 PRELIMINARY; PRT; 560 AA.
AC Q7L9G1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ12541.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK022603; BAB14122.1; -.
SQ SEQUENCE 560 AA; 61987 MW; DF0FFED7687AED74 CRC64;

Query Match 46.0%; Score 488; DB 2; Length 560;
Best Local Similarity 98.9%; Pred. No. 2e-36;
Matches 92; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy         107 MVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATA 166
               ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db           1 MVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAWKILGLFYYAALYYPLAACATA 60

Qy         167 GHTAAHLLGSTLSWAHLGVQVWQRAECPQVPKI 199
               |||||||||||||||||||||||||||||||
Db          61 GHTAAHLLGSTLSWAHLGVQVWQRAECPQVPKI 93
```

RESULT 9
Q8C442
ID Q8C442 PRELIMINARY; PRT; 137 AA.

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AC   Q8C442;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Mus musculus adult male hippocampus cDNA, RIKEN full-length enriched
DE   library, clone:C630015F10 product:stimulated by retinoic acid gene 6,
DE   full insert sequence.
GN   Name=Stra6;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hippocampus;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hippocampus;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hippocampus;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK083120; BAC38769.1; -.
DR   MGD; MGI:107742; Stra6.
DR   GO; GO:0016021; C:integral to membrane; TAS.
SQ   SEQUENCE   137 AA;  14573 MW;  27A54C974EF867CC CRC64;

  Query Match             40.2%;  Score 427;  DB 2;  Length 137;
  Best Local Similarity   66.4%;  Pred. No. 1.9e-31;
  Matches   85;  Conservative   12;  Mismatches   29;  Indels    2;  Gaps    1;

Qy          6 GNQTSPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSILVLLL 65
              |:||| | |:||| ||||:|| |  |:|||| :| |  : || | |||||||| |||||
Db          9 GSQTSSGVTDDYS--SWYIEEPLGAEEVQPEGVIPLCQLTAPPALLHACLASLSFLVLLL 66

Qy         66 LAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDEDALPF 125
              ||:|| ||:||| |     ||||||||||||    ||||||:|| |:||||||||: |||
Db         67 LALLVTRRRLWPRCGHRGLGLPSPVDFLAGDLSCTVPAAVFVVLFSNLCLLLPDENPLPF 126

Qy        126 LTLASAPS 133
               | | :| |
Db        127 LNLTAASS 134


RESULT 10
Q6DGZ6
ID   Q6DGZ6      PRELIMINARY;      PRT;   238 AA.
AC   Q6DGZ6;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Hypothetical protein (Fragment).
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC076188; AAH76188.1; -.
KW   Hypothetical protein.
FT   NON_TER     238    238
SQ   SEQUENCE   238 AA;  26788 MW;  99E960B5C4FD52B7 CRC64;

  Query Match             31.8%;  Score 337;  DB 2;  Length 238;
  Best Local Similarity   37.4%;  Pred. No. 6.5e-23;
  Matches   71;  Conservative   31;  Mismatches   74;  Indels   14;  Gaps    3;

Qy         10 SPGATEDYSYGSWYIDEPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSILVLLLLAML 69
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Db          2 SAETVNNYDYSDWY---ENAAPTKAPVEVIPPCDPTADEGLFHICIAAISLVVMLVLAIL 58

Qy         70 VRRRQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLPDEDALPFLTLA 129

Db         59 ARRQKL-SDNQRGLTGLLSPVNFLDHTQHKGLAVAVYGVLFCKLVGMVLSHHPLPFT--- 114

Qy        130 SAPSQDGKTEAPRGAWKILGLFHYAALYYPLAACATAGHTAAHLLGSTLSWAHLGVQVWQ 189

Db        115 -------KEVANKEFWMILALLYYPALYYPLLACGTLHNKVGYVLGSLLSWTHFGILVWQ 167

Qy        190 RAECPQVPKI 199

Db        168 KVDCPKTPQI 177


RESULT 11
Q7WE26
ID   Q7WE26      PRELIMINARY;      PRT;   293 AA.
AC   Q7WE26;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Putative membrane protein.
GN   OrderedLocusNames=BB4812;
OS   Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Alcaligenaceae; Bordetella.
OX   NCBI_TaxID=518;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=RB50 / ATCC BAA-588;
RX   MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA   Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA   Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA   Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA   Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA   Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA   Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA   Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA   Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA   Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA   Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT   "Comparative analysis of the genome sequences of Bordetella pertussis,
RT   Bordetella parapertussis and Bordetella bronchiseptica.";
RL   Nat. Genet. 35:32-40(2003).
DR   EMBL; BX640451; CAE35175.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR000620; DUF6.
DR   Pfam; PF00892; DUF6; 1.
KW   Complete proteome.
SQ   SEQUENCE   293 AA;  29783 MW;  E66BA78D5E88CA0C CRC64;

  Query Match             9.4%;  Score 99.5;  DB 2;  Length 293;
  Best Local Similarity   27.3%;  Pred. No. 0.58;
  Matches   50;  Conservative   17;  Mismatches   53;  Indels   63;  Gaps    9;

Qy         43 HTSIPPGLY---HACLAS--LSILVLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDR 97

Db          2 HVSALPGAQPARHAANAAGVAAILLWASLALMTATAQ----------GLP---------- 41

Qy         98 PRAVPAAVFMVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAWKIL--GLFHYAA 155

Db         42 PFQLLAASFGVAFALSAVLL------------TARRAWGRLRAPAGAWLLAVGGIFGYHA 89

Qy        156 LYY------PLAAC--------------ATAGHTAAH----LLGSTLSWAHLGVQVWQRA 191

Db         90 LYFYALGNAPVAEASLIAYLWPLLIVLFALRGAGGARRWRALAGAALGFAGTALLVWQRA 149

Qy        192 ECP 194

Db        150 GGP 152


RESULT 12
Q7W325
ID   Q7W325      PRELIMINARY;      PRT;   293 AA.
AC   Q7W325;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Putative membrane protein.
GN   OrderedLocusNames=BPP4224;
OS   Bordetella parapertussis.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Alcaligenaceae; Bordetella.
OX   NCBI_TaxID=519;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=12822 / ATCC BAA-587;
RX   MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA   Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA   Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA   Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA   Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA   Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA   Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA   Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA   Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA   Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA   Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT   "Comparative analysis of the genome sequences of Bordetella pertussis,
RT   Bordetella parapertussis and Bordetella bronchiseptica.";
RL   Nat. Genet. 35:32-40(2003).
DR   EMBL; BX640436; CAE39503.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR000620; DUF6.
DR   Pfam; PF00892; DUF6; 1.
KW   Complete proteome.
SQ   SEQUENCE   293 AA;  29769 MW;  1C52078C7FF76A0E CRC64;

  Query Match             9.1%;  Score 96.5;  DB 2;  Length 293;
  Best Local Similarity   26.8%;  Pred. No. 1.1;
  Matches   49;  Conservative   17;  Mismatches   54;  Indels   63;  Gaps    8;

Qy         43 HTSIPPGLYHACLAS-----LSILVLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGDR 97

Db          2 HVSALPGAQPARHAANGAGVAAILLWASLALMTATAQ----------GLP---------- 41

Qy         98 PRAVPAAVFMVLLSSLCLLLPDEDALPFLTLASAPSQDGKTEAPRGAWKIL--GLFHYAA 155

Db         42 PFQLLAASFGVAFALSAVLL------------TARRAWGRLRAPAGAWLLAVGGIFGYHA 89

Qy        156 LYY------PLAAC--------------ATAGHTAAH----LLGSTLSWAHLGVQVWQRA 191

Db         90 LYFYALGNAPVAEASLIAYLWPLLIVLFALRGAGGARRWRALAGAALGFAGTALLVWQRA 149

Qy        192 ECP 194

Db        150 GGP 152


RESULT 13
Q6ZNR9
ID   Q6ZNR9      PRELIMINARY;      PRT;   441 AA.
AC   Q6ZNR9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein FLJ27266.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
```

```
RC   TISSUE=Thymus;
RA   Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.,
RA   Arita M., Musashino K., Yuuki H., Hara H., Suzuki Y., Hata H.,
RA   Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA   Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B.,
RA   Nagai K., Isogai T., Sugano S.;
RL   Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK130776; BAC85426.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0004872; F:receptor activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR011009; Kinase_like.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Receptor.
SQ   SEQUENCE   441 AA;  48434 MW;  E43EDFC4753A0BB4 CRC64;

  Query Match             9.1%;  Score 96.5;  DB 2;  Length 441;
  Best Local Similarity   24.1%;  Pred. No. 1.7;
  Matches   35;  Conservative   22;  Mismatches   73;  Indels   15;  Gaps    5;

Qy          7 NQTSPGATEDYSYGSWYIDEPQ----GGXELQPEGEVPSCHT-SIPPGLYHACLASLSIL 61
              | :||     :    |:   |        ||:| |: |       |  :   || :: :|
Db        101 NNSSPALGGTFPPAPWWPPGPPPTNFSSLELEPRGQQPVAKAEGSPTAILIGCLVAIILL 160

Qy         62 VLLLLAMLVRR---RQLWPDCVRGRPGLPSPVDFLAGDRPRAVPAAVFMVLLSSLCLLLP 118
              :||::|::: |   |:|    :   |   ||   | | ||  :| :   :   |     |
Db        161 LLLIIALMLWRLHWRRLLSKVLESHPRTRSP--GLVGIRPTPLPVSPMALRCCS-----P 213

Qy        119 DEDALPFLTLASAPSQDGKTEAPRG 143
               :    |  |   | :       | |
Db        214 IQPTASFWPLTPVPLEARAPPHPPG 238


RESULT 14
Q7NIK1
ID   Q7NIK1      PRELIMINARY;      PRT;   840 AA.
AC   Q7NIK1;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Gll2182 protein.
GN   OrderedLocusNames=gll2182;
OS   Gloeobacter violaceus.
OC   Bacteria; Cyanobacteria; Chroococcales; Gloeobacter.
OX   NCBI_TaxID=33072;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=PCC 7421;
RX   MEDLINE=22977040; PubMed=14621292;
RA   Nakamura Y., Kaneko T., Sato S., Mimuro M., Miyashita H., Tsuchiya T.,
RA   Sasamoto S., Watanabe A., Kawashima K., Kishida Y., Kiyokawa C.,
RA   Kohara M., Matsumoto M., Matsuno A., Nakazaki N., Shimpo S.,
RA   Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of Gloeobacter violaceus PCC 7421, a
RT   cyanobacterium that lacks thylakoids.";
RL   DNA Res. 10:137-145(2003).
DR   EMBL; AP006575; BAC90123.1; -.
DR   HSSP; P50870; 1MR7.
DR   GO; GO:0016747; F:transferase activity, transferring groups o. . .; IEA.
DR   InterPro; IPR002656; Acyl_transf_3.
DR   InterPro; IPR003018; GAF.
DR   InterPro; IPR001451; Hexapep_transf.
DR   InterPro; IPR011004; Trimer_LpxA_like.
DR   Pfam; PF01757; Acyl_transf_3; 1.
DR   Pfam; PF01590; GAF; 1.
DR   Pfam; PF00132; Hexapep; 6.
DR   PROSITE; PS00101; HEXAPEP_TRANSFERASES; 1.
KW   Complete proteome.
SQ   SEQUENCE   840 AA;  90623 MW;  4C2A59EF60ABD838 CRC64;

  Query Match             8.5%;  Score 90.5;  DB 2;  Length 840;
  Best Local Similarity   26.2%;  Pred. No. 12;
  Matches   53;  Conservative   21;  Mismatches   65;  Indels   63;  Gaps   13;

Qy         26 EPQGGXELQPEGEVPSCHTSIPPGLYHACLASLSILVLLLLAMLVRRRQLWPDCVRGRPG 85
              ||:|    :|: : ||       |     |  |: | :|          || | :  :|
Db         14 EPRGDMTTEPKPDKPSLRLHYLDG-----LRGLTALYILFF-------HLWCD-LSFKPQ 60

Qy         86 LPSPVDFLAGD-RPRAVPAA----------VFMVLLSSLCLLLPDEDALPFLTLASAP 132
              |      |||:  |  : ||           :||| ||  ||:||
Db         61 LR-----LAGEPMPTWLQAATAWAGYGLFSVGIFMV-LSGYCLMLP----------VV 102

Qy        133 SQDGKTEA------PRGAWKILGLFHYAALYYPLAACATAGHTAAHLLG-------STLS 179
                ||:          | ||:||  : :|||   |   |  |  :   ||        :  :
Db        103 RSDGRLRGGVTGYLKRRAWRILPPY-FAALGLSLLVIALVGAGSGQSLGYMWDKAMNGFT 161

Qy        180 W----AH-LGVQVWQRAECPQV 196
              |    || | |  |  |:   :
Db        162 WEGVLAHLLLVHNWSEAQASTI 183


RESULT 15
Q7W6G2
ID   Q7W6G2      PRELIMINARY;      PRT;  2527 AA.
AC   Q7W6G2;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Putative type I polyketide synthase.
GN   Name=wcbR; OrderedLocusNames=BPP2950;
OS   Bordetella parapertussis.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC   Alcaligenaceae; Bordetella.
OX   NCBI_TaxID=519;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=12822 / ATCC BAA-587;
RX   MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA   Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA   Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA   Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA   Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA   Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA   Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA   Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA   Rabbinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA   Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA   Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT   "Comparative analysis of the genome sequences of Bordetella pertussis,
RT   Bordetella parapertussis and Bordetella bronchiseptica.";
RL   Nat. Genet. 35:32-40(2003).
CC   -!- PTM: 4'-phosphopantetheine is transferred from CoA to a specific
CC       serine of the protein (By similarity).
CC   -!- SIMILARITY: Contains 1 acyl carrier domain.
DR   EMBL; BX640432; CAE38242.1; -.
DR   HSSP; P39435; 1KAS.
DR   GO; GO:0000036; F:acyl carrier activity; IEA.
DR   GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR   GO; GO:0048037; F:cofactor binding; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0008270; F:zinc ion binding; IEA.
DR   GO; GO:0006633; P:fatty acid biosynthesis; IEA.
DR   GO; GO:0008152; P:metabolism; IEA.
DR   InterPro; IPR003231; Acyl_carrier.
DR   InterPro; IPR001227; Ac_transferase.
DR   InterPro; IPR002085; Adh_zn_family.
DR   InterPro; IPR003006; Ig_MHC.
DR   InterPro; IPR000794; Ketoacyl_synth.
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DR   InterPro; IPR006163; Phsppanteth_bind.
DR   Pfam; PF00698; Acyl_transf_1; 1.
DR   Pfam; PF00107; ADH_zinc_N; 1.
DR   Pfam; PF00109; ketoacyl-synt; 1.
DR   Pfam; PF02801; Ketoacyl-synt_C; 1.
DR   Pfam; PF00550; PP-binding; 1.
DR   ProDom; PD000887; Acyl_carrier; 1.
DR   PROSITE; PS50075; ACP_DOMAIN; 1.
DR   PROSITE; PS00606; B_KETOACYL_SYNTHASE; 1.
DR   PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW   Complete proteome; Phosphopantetheine; Transferase.
SQ   SEQUENCE   2527 AA;  269583 MW;  599CFAD9E3AE99B5 CRC64;

  Query Match             8.5%;  Score 90.5;  DB 2;  Length 2527;
  Best Local Similarity   29.0%;  Pred. No. 36;
  Matches   51;  Conservative   16;  Mismatches   66;  Indels   43;  Gaps    9;

Qy         24 IDEPQGGXELQPEGEVPSC-HTSIPPG-----LYHA----------------CLASLSI 60
              |||  :   |  |:  | :  ||  | |     : ||                  |||   :
Db       1423 IDEAERLRERCPDLSVQAIDHTEPPAGRFDLAILHANWPTLDEARQALGHVRHCLAPGGV 1482

Qy         61 LVLLLLAMLVRRRQLWPDCVRGRPGLPSPVDFLAGD-RPRAVPAAVFMVLLSSL-CL--- 115
              |:|     |  :   | | : |  |     | :|||  |   |||  :   | :| |
Db       1483 LLL-----LANQPTAWLDFIFGARG-QWWSDSVAGDATPALQPAAFWRRELQALGCACEP 1536

Qy        116 ---LLPDEDALPFL------TLASAPSQDGKTEAPRGAWKILGLFHYAALYYPLAA 162
                 |||  : |:|       |:|   | |.     |   | :|     ||:  ||||
Db       1537 AADFLPDTRSGPYLLAATVATVADGDSGDTVDAPPARRWLLLADAADAAVARPLAA 1592


Search completed: February  8, 2005, 13:40:07
Job time : 90.3473 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 13:20:30 ; Search time 144.513 Seconds
(without alignments)
869.796 Million cell updates/sec

Title: US-09-816-653A-4
Perfect score: 1695
Sequence: 1 CYISALVLSCLLTFLVLMRS.....APPTWLWESQQGFWRKKLVG 325

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1679	99.1	325	6	ABB99463	Abb99463 Amino aci
2	1134	66.9	660	5	AAU91277	Aau91277 Human NOV
3	1110.5	65.5	491	5	ABP68961	Abp68961 Human pol
4	1110.5	65.5	560	4	AAB94108	Aab94108 Human pro
5	1110.5	65.5	560	5	ABP69799	Abp69799 Human pol
6	1110.5	65.5	599	7	ADB64152	Adb64152 Human pro
7	1110.5	65.5	666	6	ABU82087	Abu82087 Novel hum
8	1110.5	65.5	667	4	AAU04557	Aau04557 Human Str
9	1110.5	65.5	667	4	AAB88572	Aab88572 Human hyd
10	1110.5	65.5	667	5	AAU83631	Aau83631 Human PRO
11	1110.5	65.5	667	5	AAU78575	Aau78575 Human Str
12	1110.5	65.5	667	5	ABB05048	Abb05048 Human NOV
13	1110.5	65.5	667	5	AAO19413	Aao19413 Human mol
14	1110.5	65.5	667	6	ABU80778	Abu80778 Human PRO
15	1110.5	65.5	667	6	ABO33744	Abo33744 Novel hum
16	1110.5	65.5	667	6	ABJ72267	Abj72267 Human PRO
17	1110.5	65.5	667	6	ABJ72395	Abj72395 Human PRO
18	1110.5	65.5	667	6	ABO34290	Abo34290 Human sec
19	1110.5	65.5	667	7	ABJ72097	Abj72097 Human mem
20	1110.5	65.5	667	7	ADB83570	Adb83570 Novel hum
21	1110.5	65.5	667	7	ADB80676	Adb80676 Novel hum
22	1110.5	65.5	667	7	ADB73217	Adb73217 Novel hum
23	1110.5	65.5	667	7	ADB78299	Adb78299 Novel hum
24	1110.5	65.5	667	7	ADB84947	Adb84947 Human PRO
25	1110.5	65.5	667	7	ADB78053	Adb78053 Novel hum
26	1110.5	65.5	667	7	ADB87119	Adb87119 Human PRO
27	1110.5	65.5	667	7	ADB84701	Adb84701 Human PRO
28	1110.5	65.5	667	7	ADB83816	Adb83816 Novel hum
29	1110.5	65.5	667	7	ADB72971	Adb72971 Novel hum
30	1110.5	65.5	667	7	ADC36809	Adc36809 Human PRO
31	1110.5	65.5	667	7	ADC21799	Adc21799 Human PRO
32	1110.5	65.5	667	7	ADC49830	Adc49830 Novel hum
33	1110.5	65.5	667	7	ADC49029	Adc49029 Novel hum
34	1110.5	65.5	667	7	ADC49546	Adc49546 Novel hum
35	1110.5	65.5	667	7	ADC47407	Adc47407 Novel hum
36	1110.5	65.5	667	7	ADC47152	Adc47152 Novel hum
37	1110.5	65.5	667	7	ADC78027	Adc78027 Novel hum
38	1110.5	65.5	667	7	ADD06262	Add06262 Novel hum
39	1110.5	65.5	667	7	ADC77781	Adc77781 Novel hum
40	1110.5	65.5	667	7	ADD50744	Add50744 Novel hum
41	1110.5	65.5	667	7	ADD50990	Add50990 Novel hum
42	1110.5	65.5	667	7	ADD50471	Add50471 Human PRO
43	1110.5	65.5	667	7	ADD50225	Add50225 Human PRO
44	1110.5	65.5	667	7	ADD51236	Add51236 Novel hum
45	1110.5	65.5	667	8	ADC48783	Adc48783 Novel hum

ALIGNMENTS

RESULT 1
ABB99463
ID ABB99463 standard; protein; 325 AA.
XX
AC ABB99463;
XX
DT 12-FEB-2003 (first entry)
XX
DE Amino acid sequence of the carboxy-terminal of human STRA6.
XX
KW Human; STRA6; retinoic acid; hSTRA6; Wnt-1; cellular transformation;
KW tumour; colon cancer; breast cancer; melanoma; gene therapy.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 146
FT /note= "unknown amino acid encoded by GNN"
FT Misc-difference 147
FT /note= "unknown amino acid encoded by NNN"
FT Misc-difference 148
FT /note= "unknown amino acid encoded by NCC"
FT Misc-difference 213
FT /note= "Gly encoded by GG"
FT Misc-difference 232
FT /note= "unknown amino acid encoded by ANG"
FT Misc-difference 290
FT /note= "unknown amino acid encoded by NGT"
FT Misc-difference 292
FT /note= "unknown amino acid encoded by TNG"
FT Misc-difference 302
FT /note= "unknown amino acid encoded by CAN"
FT Misc-difference 303
FT /note= "unknown amino acid encoded by GAN"
XX
PN WO200277027-A1.
XX
PD 03-OCT-2002.
XX
PF 23-MAR-2001; 2001WO-US009561.
XX
PR 23-MAR-2000; 2000US-0191532P.
XX
PA (CURA-) CURAGEN CORP.
PA (GETH) GENENTECH INC.
XX
PI Rastelli LK, Pennica D;
XX

DR WPI; 2003-058366/05.
DR N-PSDB; ABV76853.
XX
PT New human STRA6 (stimulated by retinoic acid) proteins and nucleic acids
PT encoding the proteins, useful for treating cancers (e.g. colon and breast
PT cancer, or melanoma), or in gene therapy.
XX
PS Claim 4; Page 11-13; 113pp; English.
XX
CC The present sequence represents the carboxy-terminal portion of a human
CC protein, designated STRA6 (stimulated by retinoic acid). hSTRA6 (human
CC STRA6) is modulated by Wnt-1 and plays a role in cellular transformation.
CC The hSTRA6 nucleic acids and proteins are useful for treating tumours
CC (e.g. colon and breast cancer, or melanoma), in gene therapy, in
CC diagnostic applications where the presence or amount of the nucleic acid
CC or protein is to be assessed, and in the generation of antibodies that
CC bind immunospecifically to these sequences for therapeutic and diagnostic
CC applications. hSTRA6 nucleic acid fragments may be used as hybridization
CC probes to identify hSTRA6-encoding nucleic acids, or as PCR primers for
CC amplification and/or mutation of hSTRA6 molecules
XX
SQ Sequence 325 AA;

Query Match 99.1%; Score 1679; DB 6; Length 325;
Best Local Similarity 100.0%; Pred. No. 5.3e-166;
Matches 325; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 CYISALVLSCLLTFLVLMRSLVTHRLGSGGSGDGQFSWNLFSVPLPLPPLAGLLVQQIIF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CYISALVLSCLLTFLVLMRSLVTHRLGSGGSGDGQFSWNLFSVPLPLPPLAGLLVQQIIF 60

Qy         61 FLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVILQNMAAHWVFLETHDGHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVILQNMAAHWVFLETHDGHP 120

Qy        121 QLTNRRVLYAATFLLFPLNVLVGAMXXXCSPSIAIRHPTPGYYTYRNFLKIEVSQSHPAM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QLTNRRVLYAATFLLFPLNVLVGAMXXXCSPSIAIRHPTPGYYTYRNFLKIEVSQSHPAM 180

Qy        181 TAFCSLLLQAQSLLPRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TAFCSLLLQAQSLLPRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGL 240

Qy        241 AYTLLHNPTLQVFRKTALLGANGAQPCSSLPGSPPSITPAMQPAGPPDHXGXVEVCLHWE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AYTLLHNPTLQVFRKTALLGANGAQPCSSLPGSPPSITPAMQPAGPPDHXGXVEVCLHWE 300

Qy        301 PXXGSAPPTWLWESQQGFWRKKLVG 325
              |||||||||||||||||||||||||
Db        301 PXXGSAPPTWLWESQQGFWRKKLVG 325
```

RESULT 2
AAU91277
ID AAU91277 standard; protein; 660 AA.
XX
AC AAU91277;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human NOV2a protein.
XX
KW Human; NOVX; gene therapy; cardiomyopathy; atherosclerosis; diabetes;
KW cell signal processing; metabolic pathway modulation; inflammation;
KW autoimmune disorder; scleroderma; transplantation; allergy;
KW systemic lupus erythematosus; haemophilia; Alzheimer's disease;
KW graft versus host disease; Lesch-Nyhan syndrome; periodontitis;
KW pancreatitis; musculoskeletal disorder; Parkinson's disease;
KW Huntington's disease; behavioural disorder; pain; obesity; wound healing;
KW neurodegenerative disorder; neuropsychiatric disorder; hypertension;
KW growth disorder; reproductive disorder; lung disease.
XX
OS Homo sapiens.

XX
PN WO200216600-A2.
XX
PD 28-FEB-2002.
XX
PF 27-AUG-2001; 2001WO-US026518.
XX
PR 25-AUG-2000; 2000US-0227800P.
PR 25-AUG-2000; 2000US-0228205P.
PR 25-AUG-2000; 2000US-0228324P.
PR 30-AUG-2000; 2000US-0228997P.
PR 30-AUG-2000; 2000US-0229185P.
PR 01-SEP-2000; 2000US-0229780P.
PR 01-SEP-2000; 2000US-0229848P.
PR 01-SEP-2000; 2000US-0229850P.
PR 22-JAN-2001; 2001US-0263337P.
PR 31-JAN-2001; 2001US-0265518P.
PR 15-MAR-2001; 2001US-0276451P.
PR 27-MAR-2001; 2001US-0279196P.
PR 24-AUG-2001; 2001US-00939398.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Gerlach V, Macdougall JR, Smithson G, Stone DJ, Ellerman K;
PI Spytek KA, Zerhusen BD, Rastelli L, Verney CAM, Patturajan M;
PI Tchernev VT, Padigaru M, Taupier RJ;
XX
DR WPI; 2002-292064/33.
DR N-PSDB; ABK55561.
XX
PT New isolated cytoplasmic, nuclear, membrane bound and secreted
PT polypeptides, termed NOVX, useful for treating inflammation, autoimmune
PT disorders, hemophilia, Lesch-Nyhan syndrome, pancreatitis,
PT musculoskeletal disorders.
XX
PS Claim 1; Page 18; 245pp; English.
XX
CC The invention relates to an isolated cytoplasmic, nuclear, membrane bound
CC or secreted polypeptide, designated NOVX (actually NOV1, 2a, 2b, 3a, 3b,
CC 4, 5a, 5b, 5c, 5d, 5e, 5f, 5g, 5h, 5i, 6, 7 and 8), a variant of NOVX, a
CC mature form, or a variant of the mature form of NOVX. Also included are a
CC polynucleotide encoding NOVX (or its complement), a vector comprising the
CC polynucleotide, a cell comprising the vector, an anti-NOVX antibody,
CC determining the presence of NOVX in a sample using the antibody,
CC determining the presence of NOVX polynucleotide in a sample using a probe
CC which binds to NOVX polynucleotide, identifying a an agent which binds to
CC NOVX (including modulators of NOVX). NOVX, the polynucleotide and the
CC antibody are useful for diagnosing, treating or preventing a NOVX-
CC associated disorder selected from cardiomyopathy, atherosclerosis,
CC diabetes, a disorder related to cell signal processing and metabolic
CC pathway modulation, inflammation, autoimmune disorders, scleroderma,
CC transplantation, allergies, systemic lupus erythematosus, haemophilia,
CC graft versus host disease, Alzheimer's disease, stroke, Lesch-Nyhan
CC syndrome, periodontitis, pancreatitis, musculoskeletal disorders,
CC Parkinson's disease, Huntington's disease, behavioural disorders, pain,
CC neurodegenerative and neuropsychiatric disorders, hypertension, wound
CC healing, obesity, growth and reproductive disorders, lung diseases and
CC many other diseases and disorders listed in the specification. NOVX, the
CC polynucleotide and the antibody are useful in screening assays, detection
CC assays (e.g., chromosomal mapping, tissue typing, forensic biology),
CC predictive medicine (e.g., diagnostic assays, prognostic assays,
CC monitoring clinical trials and pharmacogenomic), and in methods of
CC treatment (e.g., therapeutic and prophylactic). NOVX is useful as
CC immunogen to produce antibodies immunospecific for NOVX, as vaccines to
CC screen for potential agonist and antagonist compounds, and as bait
CC protein in a two-hybrid or three-hybrid assay. The polynucleotide is
CC useful in gene therapy, to express NOVX, to detect NOVX mRNA or a genetic
CC lesion in a NOVX gene, and to modulate NOVX activity. The vector is
CC useful for producing non-human transgenic animals. The antibody is useful
CC for isolating, and purifying NOVX and to monitor protein levels in tissue
CC as part of a clinical testing procedure. The present sequence represents
CC a NOVX protein
XX

```
SQ   Sequence 660 AA;

  Query Match             66.9%;  Score 1134;  DB 5;  Length 660;
  Best Local Similarity   76.9%;  Pred. No. 8.4e-109;
  Matches  237;  Conservative    4;  Mismatches   25;  Indels   42;  Gaps    5;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD-------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |               | |  ||
Db        353 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 412

Qy         43 VPLP-----LPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTL 97
              |||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        413 AYQTAFICLLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTL 472

Qy         98 ALAVILQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC-------- 149
              ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        473 ALAVILQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALY 532

Qy        150 ------SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTM 198
                  :::  |      ||||||||||||||||||||||||||||||||||||||||||
Db        533 NAIHLGQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTM 592

Qy        199 AAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTAL 258
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        593 AAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTAL 652

Qy        259 LGANGAQP 266
              ||||||||
Db        653 LGANGAQP 660
```

```
RESULT 3
ABP68961
ID   ABP68961 standard; protein; 491 AA.
XX
AC   ABP68961;
XX
DT   20-JAN-2003  (first entry)
XX
DE   Human polypeptide SEQ ID NO 1008.
XX
KW   Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW   cell-proliferative disorder; neurodegenerative disease; bacterial;
KW   Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW   multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW   arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW   antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW   haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
KW   antiarthritic.
XX
OS   Homo sapiens.
XX
PN   WO200270539-A2.
XX
PD   12-SEP-2002.
XX
PF   05-MAR-2002; 2002WO-US005095.
XX
PR   05-MAR-2001; 2001US-00799451.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Zhou P,  Goodrich RW,  Asundi V,  Zhang J,  Zhao QA,  Ren F;
PI   Xue AJ,  Yang Y,  Ma Y,  Yamazaki V,  Chen R,  Wang Z,  Ghosh M;
PI   Wehrman T,  Wang J,  Wang D,  Drmanac RT;
XX
DR   WPI; 2002-759812/82.
DR   N-PSDB; ABZ11178.
XX
PT   New polynucleotides comprising sequences assembled from expressed
PT   sequence tags (ESTs), useful for treating cell-proliferative,
PT   neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT   or coagulation disorders.
XX
PS   Claim 9; SEQ ID NO 1008; 1012pp + Sequence Listing; English.
XX
CC   The invention relates to an isolated polynucleotide (I) comprising a
CC   nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC   ABZ12066) or their mature protein coding portion, active domain coding
CC   protein or complementary sequences. The polynucleotides are useful for
CC   identifying expressed genes or for physical mapping of human genome. The
CC   encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC   markers, as a food supplement, for generating antibodies, in medical
CC   imaging, screening and diagnostic assays and for treating cell-
CC   proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC   or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC   diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC   platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC   or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC   arthritis, etc. Note: The sequence data for this patent did not form part
CC   of the printed specification, but was obtained in electronic format
CC   directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ   Sequence 491 AA;

  Query Match             65.5%;  Score 1110.5;  DB 5;  Length 491;
  Best Local Similarity   76.6%;  Pred. No. 1.6e-106;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD-------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |               | |  ||
Db        189 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 248

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                  |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        249 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 308

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              |||||||||||||||||||||||||||||||||||||||||||||||
Db        309 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 368

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                   :::  |      ||||||||||||||||||||||||||||||||||||||||||||
Db        369 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 428

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        429 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 488

Qy        264 AQP 266
              |||
Db        489 AQP 491
```

```
RESULT 4
AAB94108
ID   AAB94108 standard; protein; 560 AA.
XX
AC   AAB94108;
XX
DT   26-JUN-2001  (first entry)
XX
DE   Human protein sequence SEQ ID NO:14340.
XX
KW   Human; primer; detection; diagnosis; antisense therapy; gene therapy.
XX
OS   Homo sapiens.
XX
PN   EP1074617-A2.
XX
PD   07-FEB-2001.
XX
PF   28-JUL-2000; 2000EP-00116126.
XX
PR   29-JUL-1999;   99JP-00248036.
PR   27-AUG-1999;   99JP-00300253.
```

PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX
PA (HELI-) HELIX RES INST.
XX
PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX
DR WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 14340; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesising 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dT primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 560 AA;

```
  Query Match             65.5%;  Score 1110.5;  DB 4;  Length 560;
  Best Local Similarity   76.6%;  Pred. No. 1.9e-106;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD-------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |             | |  ||
Db        258 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 317

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
              |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        318 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 377

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------ 149
              |||||||||||||||||||||||||||||||||||||||||||
Db        378 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 437

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                 :::  |      ||||||||||||||||||||||||||||||||||||||||||||
Db        438 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 497

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        498 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 557

Qy        264 AQP 266
              |||
Db        558 AQP 560
```

RESULT 5

ABP69799
ID ABP69799 standard; protein; 560 AA.
XX
AC ABP69799;
XX
DT 20-JAN-2003 (first entry)
XX
DE Human polypeptide SEQ ID NO 1846.
XX
KW Human; genome mapping; gene therapy; food supplement; virus; fungus;
KW cell-proliferative disorder; neurodegenerative disease; bacterial;
KW Parkinson's disease; Alzheimer's disease; autoimmune disease;
KW multiple sclerosis; diabetes; genetic disorder; wound; burn; infection;
KW arthritis; cytostatic; immunomodulator; nootropic; neuroprotective;
KW antiparkinsonian; antidiabetic; immunosuppressive; dermatological;
KW haemostatic; vulnerary; fungicide; antibacterial; virucide; protozoacide;
KW antiarthritic.
XX
OS Homo sapiens.
XX
PN WO200270539-A2.
XX
PD 12-SEP-2002.
XX
PF 05-MAR-2002; 2002WO-US005095.
XX
PR 05-MAR-2001; 2001US-00799451.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Zhou P, Goodrich RW, Asundi V, Zhang J, Zhao QA, Ren F;
PI Xue AJ, Yang Y, Ma Y, Yamazaki V, Chen R, Wang Z, Ghosh M;
PI Wehrman T, Wang J, Wang D, Drmanac RT;
XX
DR WPI; 2002-759812/82.
DR N-PSDB; ABZ12016.
XX
PT New polynucleotides comprising sequences assembled from expressed
PT sequence tags (ESTs), useful for treating cell-proliferative,
PT neurodegenerative, autoimmune, genetic, myeloid or lymphoid, or platelet
PT or coagulation disorders.
XX
PS Claim 9; SEQ ID NO 1846; 1012pp + Sequence Listing; English.
XX
CC The invention relates to an isolated polynucleotide (I) comprising a
CC nucleotide sequence selected from any of 948 sequences (ABZ11119-
CC ABZ12066) or their mature protein coding portion, active domain coding
CC protein or complementary sequences. The polynucleotides are useful for
CC identifying expressed genes or for physical mapping of human genome. The
CC encoded polypeptides (ABP68902-ABP69849) are useful as molecular weight
CC markers, as a food supplement, for generating antibodies, in medical
CC imaging, screening and diagnostic assays and for treating cell-
CC proliferative disorders (cancer), neurodegenerative diseases (Parkinson's
CC or Alzheimer's disease), autoimmune diseases (multiple sclerosis,
CC diabetes, lupus) genetic disorders, myeloid or lymphoid disorders,
CC platelet or coagulation disorders, wound, burns, incision, ulcers, liver
CC or lung fibrosis, infections (bacterial, viral, fungal, parasitic),
CC arthritis, etc. Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 560 AA;

```
  Query Match             65.5%;  Score 1110.5;  DB 5;  Length 560;
  Best Local Similarity   76.6%;  Pred. No. 1.9e-106;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD-------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |             | |  ||
Db        258 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 317

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
              |||||||||||||||||||||||||||||| ||||||||||||||||||
```

```
Db        318 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 377

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------ 149
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        378 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 437

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                  :::  |      ||||||||||||||||||||||||||||||||||||||||||||||
Db        438 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 497

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        498 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 557

Qy        264 AQP 266
              |||
Db        558 AQP 560
```

RESULT 6
ADB64152
ID ADB64152 standard; protein; 599 AA.
XX
AC ADB64152;
XX
DT 04-DEC-2003 (first entry)
XX
DE Human protein encoded by clone CTONG20041260.
XX
KW Human; pharmaceutical; diagnostic; gene therapy; tissue regeneration;
KW cell regeneration; membrane protein; signal transduction-related protein;
KW transcription-related protein; osteoporosis; neurological disease;
KW cancer; tumour.
XX
OS Homo sapiens.
XX
PN EP1308459-A2.
XX
PD 07-MAY-2003.
XX
PF 28-MAR-2002; 2002EP-00007401.
XX
PR 05-NOV-2001; 2001JP-00379298.
PR 25-JAN-2002; 2002US-00350978.
XX
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
XX
PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;
XX
DR WPI; 2003-450961/43.
DR N-PSDB; ADB62182.
XX
PT New polynucleotides and polypeptides, useful for developing a diagnostic
PT marker or medicines for regulation of their expression and activity, or
PT as targets of gene therapy.
XX
PS Claim 1; Page; 222pp; English.
XX
CC The invention discloses a polynucleotide comprising a sequence selected
CC from 1970 fully defined nucleotide sequences which encode novel
CC polypeptides. Also claimed is a polypeptide encoded by the polynucleotide
CC or its partial peptide, an antibody binding to the polypeptide or peptide
CC of the polynucleotide, immunologically assaying the polypeptide or
CC peptide of the polynucleotide by contacting the polypeptide or peptide
CC with the antibody of the encoded protein, and observing the binding
CC between the two, a transformant carrying the polynucleotide in an
CC expressible manner and an antisense polynucleotide. The oligonucleotide
CC is useful as a primer for synthesising the polynucleotide, or as a probe
CC for detecting the polynucleotide. The polynucleotides and encoded
CC proteins are useful as pharmaceutical agents and many disease-related
CC genes may be included in them, for developing a diagnostic marker or
CC medicines for regulation of their expression and activity, or as targets
CC of gene therapy. The genes are involved in tissue and/or cell
CC regeneration. Membrane proteins, signal transduction-related proteins,
CC transcription-related proteins, disease-related proteins and genes
CC encoding them can be used as indicators for diseases (e.g. osteoporosis,
CC neurological diseases, cancer, tumours. The cDNA may be used to regulate
CC the activity or expression of the encoded protein to treat diseases. The
CC sequence presented is a protein of the invention. Note: Some of the
CC sequence data for this patent is not represented in the printed
CC specification, but is based on sequence information supplied by the
CC European Patent Office.
XX
SQ Sequence 599 AA;

```
  Query Match             65.5%;  Score 1110.5;  DB 7;  Length 599;
  Best Local Similarity   76.6%;  Pred. No. 2.1e-106;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD-------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |             | |  ||
Db        297 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 356

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                      |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        357 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 416

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------ 149
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        417 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 476

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                  :::  |      ||||||||||||||||||||||||||||||||||||||||||||||
Db        477 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 536

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        537 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 596

Qy        264 AQP 266
              |||
Db        597 AQP 599
```

RESULT 7
ABU82087
ID ABU82087 standard; protein; 666 AA.
XX
AC ABU82087;
XX
DT 26-JUN-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO10282.
XX
KW Human; secreted and transmembrane protein; PRO; cardiant; cytostatic;
KW antiangiogenic; hypotensive; vulnenry; antiarteriosclerotic;
KW gene therapy; cardiovascular disorder; endothelial disorder;
KW angiogenic disorder; cardiac hypertrophy; trauma; cancer;
KW age-related macular degeneration; atherosclerosis; hypertension;
KW arterial restenosis; rheumatoid arthritis; angina; myocardial infarction;
KW thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma;
KW liver carcinoma; wound healing; chromosome mapping; gene mapping.
XX
OS Homo sapiens.
XX
PN US2003088063-A1.
XX
PD 08-MAY-2003.
XX
PF 12-AUG-2002; 2002US-00219003.
XX
PR 25-JUL-2000; 2000US-0220664P.
PR 01-JUN-2001; 2001WO-US017800.

PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-393229/37.
XX
PT One hundred and eighty seven nucleic acids encoding PRO polypeptides,
PT useful in diagnosis and treatment of cardiovascular (e.g. myocardial
PT infarction), endothelial or angiogenic disorders in a mammal.
XX
PS Claim 11; Fig 80; 314pp; English.
XX
CC The invention describes one hundred and eighty seven nucleic acids
CC encoding novel human secreted and transmembrane (PRO) polypeptides. The
CC PRO nucleic acids, polypeptides, agonists and antagonists are useful for
CC treating or diagnosing a cardiovascular, endothelial or angiogenic
CC disorder in a mammal, e.g. cardiac hypertrophy, trauma, cancer, age-
CC related macular degeneration, atherosclerosis, hypertension, arterial
CC restenosis, rheumatoid arthritis, angina, myocardial infarctions,
CC thrombophlebitis, lymphangitis, tumour angiogenesis (such as breast
CC carcinoma and liver carcinoma) and wound healing. The PRO nucleic acids
CC have applications in molecular biology, including use as hybridisation
CC probes, and in chromosome and gene mapping. This is the amino acid
CC sequence of a novel human secreted and transmembrane PRO polypeptide
XX
SQ Sequence 666 AA;

Query Match 65.5%; Score 1110.5; DB 6; Length 666;
Best Local Similarity 76.6%; Pred. No. 2.4e-106;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

```
Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |              | |  ||
Db        364 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 423

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                  |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        424 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 483

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------ 149
              |||||||||||||||||||||||||||||||||||||||||||||
Db        484 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 543

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                  :::  |      |||||||||||||||||||||||||||||||||||||||||||
Db        544 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 603

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        604 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 663

Qy        264 AQP 266
              |||
Db        664 AQP 666
```

RESULT 8
AAU04557
ID AAU04557 standard; protein; 667 AA.
XX
AC AAU04557;
XX
DT 26-SEP-2001 (first entry)
XX
DE Human Stra6 homologue, PRO10282.
XX
KW Human; Stra6; PRO10282; 15q23; tumour; breast cancer; head tumour;
KW leukaemia; lymphoid malignancy; inflammatory disorder;
KW immunogenic disorder; antigen; antibody.
XX
OS Homo sapiens.
XX

FH	Key	Location/Qualifiers
FT	Modified-site	8. .12
FT		/note= "Asn is N-glycosylated"
FT	Region	50. .56
FT		/label= N_myristoylation_site
FT	Domain	54. .69
FT		/label= Transmembrane_domain
FT	Region	89. .97
FT		/note= "Region deleted in Stra6 variant PRO19578"
FT	Domain	102. .119
FT		/label= Transmembrane_domain
FT	Region	132. .140
FT		/note= "ATP/GTP-binding site motif A (P-loop)"
FT	Domain	148. .166
FT		/label= Transmembrane_domain
FT	Region	176. .182
FT		/label= N_myristoylation_site
FT	Domain	207. .222
FT		/label= Transmembrane_domain
FT	Region	241. .247
FT		/label= N_myristoylation_site
FT	Domain	301. .320
FT		/label= Transmembrane_domain
FT	Region	317. .323
FT		/label= N_myristoylation_site
FT	Region	341. .347
FT		/label= N_myristoylation_site
FT	Domain	364. .380
FT		/label= Transmembrane_domain
FT	Region	364. .375
FT		/note= "Prokaryotic membrane lipoprotein attachment site"
FT	Domain	431. .451
FT		/label= Transmembrane_domain
FT	Domain	474. .489
FT		/label= Transmembrane_domain
FT	Region	525. .531
FT		/label= N_myristoylation_site
FT	Domain	560. .535
FT		/label= Transmembrane_domain
FT	Region	627. .633
FT		/label= N_myristoylation_site
FT	Region	631. .637
FT		/label= N_myristoylation_site
FT	Region	640. .646
FT		/label= N_myristoylation_site
FT	Region	661. .667
FT		/label= N_myristoylation_site

XX
PN WO200151635-A2.
XX
PD 19-JUL-2001.
XX
PF 11-JAN-2001; 2001WO-US000847.
XX
PR 13-JAN-2000; 2000US-0175849P.
PR 14-APR-2000; 2000US-0197089P.
PR 29-AUG-2000; 2000US-0228914P.
XX
PA (GETH) GENENTECH INC.
XX
PI Pennica D, Smith V, Wood WI;
XX
DR WPI; 2001-442146/47.
DR N-PSDB; AAS08630.
XX
PT Human nucleic acid encoding a PRO10282 or PRO19578 polypeptide (the PRO
PT polypeptides are referred to as Stra6 polypeptides), useful in molecular
PT biology, including use as hybridization probes, and in chromosome and
PT gene mapping.
XX

```
PS   Claim 24; Fig 2; 159pp; English.
XX
CC   The sequence is human PRO10282, a homologue of murine Stra6, a retinoic
CC   acid responsive protein thought to play an important role in early
CC   dorsoventral limb patterning during development and later in the control
CC   of endochondral ossification. The gene for the Stra6 homologue is located
CC   on chromosome 15q23. The Stra6 polypeptides, agonists, antagonists or
CC   anti-Stra6 antibodies are useful for preparation of a medicament useful
CC   in the treatment of a condition which is responsive to the Stra6
CC   polypeptides, agonists, antagonists or anti-Stra6 antibodies. The Stra6
CC   polypeptides may also be employed as molecular weight markers for protein
CC   electrophoresis. The Stra6 nucleic acids have applications in molecular
CC   biology, including use as hybridisation probes, and in chromosome and
CC   gene mapping. The antibodies and other anti-tumour compounds may be used
CC   to treat various conditions, including those characterised by
CC   overexpression and/or activation of amplified genes. Exemplary conditions
CC   or disorders include benign or malignant tumours (e.g., renal, liver,
CC   kidney, bladder, breast, gastric, ovarian, colorectal, prostate,
CC   pancreatic, lung, vulval, thyroid, hepatic carcinomas, sarcomas,
CC   glioblastomas, and various head and neck tumours, leukaemias and lymphoid
CC   malignancies), neuronal, glial, astrocytal, hypothalamic and other
CC   glandular, macrophagal, epithelial, stromal and blastocoelic disorders,
CC   inflammatory, angiogenic and immunogenic disorders
XX
SQ   Sequence 667 AA;

  Query Match             65.5%;  Score 1110.5;  DB 4;  Length 667;
  Best Local Similarity   76.6%;  Pred. No. 2.4e-106;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |              | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              ||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                  :::  |      ||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667


RESULT 9
AAB88572
ID   AAB88572 standard; protein; 667 AA.
XX
AC   AAB88572;
XX
DT   04-JUN-2001  (first entry)
XX
DE   Human hydrophobic domain containing protein clone HP10713 #36.
XX
KW   Human; hydrophobic domain; immunosuppressant; anti-HIV; neuroprotective;
KW   antianaemic; vulnerary; antiulcer; osteopathic; anti-inflammatory;
KW   cytostatic; gene therapy; autoimmune disorder; multiple sclerosis;
KW   HIV infection; anaemia; burn; ulcer; osteoporosis; tumour; wound healing;
KW   inflammatory bowel disease; nutritional supplement; appetite; vaccine;
KW   behavioural characteristic; immune response.
XX
OS   Homo sapiens.
XX
PN   WO200112660-A2.
XX
PD   22-FEB-2001.
XX
PF   10-AUG-2000; 2000WO-JP005356.
XX
PR   17-AUG-1999;   99JP-00230344.
PR   07-SEP-1999;   99JP-00252551.
PR   01-OCT-1999;   99JP-00281132.
PR   22-OCT-1999;   99JP-00301624.
PR   04-NOV-1999;   99JP-00313877.
XX
PA   (SAGA ) SAGAMI CHEM RES CENT.
PA   (PROT-) PROTEGENE INC.
XX
PI   Kato S,  Kimura T;
XX
DR   WPI; 2001-160059/16.
DR   N-PSDB; AAF94442.
XX
PT   Human proteins with hydrophobic domains and the DNAs which encode them
PT   are useful for treating autoimmune disorders, burns and tumors and for
PT   screening novel pharmaceuticals.
XX
PS   Claim 1; Page 288-291; 518pp; English.
XX
CC   AAF94417 to AAF94516 encode the human proteins given in AAB88557 to
CC   AAB88606 (I) which have a hydrophobic domain. (I) have immunosuppressant,
CC   anti-HIV, neuroprotective, antianaemic, vulnerary, antiulcer,
CC   osteopathic, anti-inflammatory and cytostatic activities, and can be used
CC   in gene therapy. (I) can be used as pharmaceuticals and as antigens to
CC   prepare antibodies. DNA and cDNA (II) encoding (I) can be used as probes
CC   for genetic diagnosis and gene sources for gene therapy or for producing
CC   (I) in large quantities. Cells containing (II) are used for the detection
CC   of ligands or receptors corresponding to membrane or secretory proteins
CC   and to screen small molecule novel pharmaceuticals. Antibodies directed
CC   to (I) can be used for the detection, quantification and purification of
CC   (I). Activities of (I) may include cytokine and cell
CC   proliferation/differentiation function, immune stimulating or suppressing
CC   activity, haematopoiesis regulating activity, tissue growth activity,
CC   activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC   and thrombolytic activity, receptor/ligand activity and anti-inflammatory
CC   activity. (I) and (II) can be used to treat autoimmune disorders e.g.
CC   multiple sclerosis, HIV infections, anaemia, burns, ulcers, osteoporosis,
CC   inflammatory bowel disease and tumours. (I) and (II) can also be used for
CC   wound healing, as nutritional sources or supplements e.g. as amino acid,
CC   carbon or nitrogen source, to effect metabolism, catabolism, anabolism,
CC   processing and utilisation of dietary fat, protein, carbohydrate,
CC   vitamins and minerals, to effect behavioural characteristics, to affect
CC   appetite, and can act as antigens in vaccines to raise an immune response
CC   to the protein or another material cross-reactive with the protein
XX
SQ   Sequence 667 AA;

  Query Match             65.5%;  Score 1110.5;  DB 4;  Length 667;
  Best Local Similarity   76.6%;  Pred. No. 2.4e-106;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |              | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              ||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                  :::  |      ||||||||||||||||||||||||||||||||||||||||||||
```

```
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667
```

RESULT 10
AAU83631
ID AAU83631 standard; protein; 667 AA.
XX
AC AAU83631;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human PRO protein, Seq ID No 80.
XX
KW Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
KW breast cancer; prostate tumour; rectal tumour; liver tumour;
KW pericyte cell proliferation; chondrocyte cell proliferation;
KW tumour necrosis factor-alpha.
XX
OS Homo sapiens.
XX
PN WO200208288-A2.
XX
PD 31-JAN-2002.
XX
PF 29-JUN-2001; 2001WO-US021066.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220585P.
PR 25-JUL-2000; 2000US-0220605P.
PR 25-JUL-2000; 2000US-0220607P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220638P.
PR 25-JUL-2000; 2000US-0220664P.
PR 25-JUL-2000; 2000US-0220666P.
PR 26-JUL-2000; 2000US-0220893P.
PR 28-JUL-2000; 2000WO-US020710.
PR 01-AUG-2000; 2000US-0222425P.
PR 22-AUG-2000; 2000US-0227133P.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 10-NOV-2000; 2000WO-US030873.
PR 28-NOV-2000; 2000US-0253646P.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 22-MAR-2001; 2001US-00816744.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001WO-US017092.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2002-172001/22.
DR N-PSDB; ABK33575.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for treating a PRO related disorder and for diagnosing tumors such
PT as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
PT or liver tumor.
XX
PS Claim 11; Fig 80; 359pp; English.
XX
CC The invention relates to one hundred and twenty two nucleic acids
CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
CC agonists and antagonists are useful for treating a PRO related disorder.
CC The PRO polypeptides are useful for diagnosing tumours, especially lung
CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
CC liver tumour. The PRO polypeptides are useful for stimulating the
CC proliferation of, or gene expression, in pericyte cells, for stimulating
CC the proliferation or differentiation of chondrocyte cells, for
CC stimulating the release of tumour necrosis factor-alpha from human blood,
CC for stimulating or inhibiting the proliferation of normal human dermal
CC fibroblast cells. The PRO polypeptide may also be used as molecular
CC weight markers and for tissue typing. The PRO nucleic acids have
CC applications in molecular biology, including use as hybridisation probes,
CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
CC protein sequences of the invention
XX
SQ Sequence 667 AA;

Query Match 65.5%; Score 1110.5; DB 5; Length 667;
Best Local Similarity 76.6%; Pred. No. 2.4e-106;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

```
Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |                | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                  |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------ 149
              ||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                   :::  |      ||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667
```

RESULT 11
AAU78575
ID AAU78575 standard; protein; 667 AA.
XX
AC AAU78575;
XX
DT 18-JUN-2002 (first entry)
XX
DE Human Stra6 (PRO10282) protein.
XX
KW Human; cancer; Stra6; PRO10282; cytostatic; stromal disorder; tumour;
KW retinoid; Wnt; tumour antigen; leukaemia; lymphoid malignancy;
KW neuronal disorder; glial disorder; astrocytal disorder;
KW hypothalamic disorder; glandular disorder; macrophagal disorder;
KW epithelial disorder; blastocoelic disorder; chromosome 15q23.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Region 8. .12
FT /note= "N Glycosylation site"
FT Region 50. .56
FT /note= "N-myristoylation site"

```
FT   Domain          54. .69
FT                   /note= "Transmembrane domain"
FT   Domain          102. .119
FT                   /note= "Transmembrane domain"
FT   Region          132. .140
FT                   /note= "ATP/GTP binding site motif A"
FT   Domain          148. .166
FT                   /note= "Transmembrane domain"
FT   Region          176. .182
FT                   /note= "N-myristoylation site"
FT   Domain          207. .222
FT                   /note= "Transmembrane domain"
FT   Region          241. .247
FT                   /note= "N-myristoylation site"
FT   Domain          301. .320
FT                   /note= "Transmembrane domain"
FT   Region          317. .323
FT                   /note= "N-myristoylation site"
FT   Region          341. .347
FT                   /note= "N-myristoylation site"
FT   Domain          364. .380
FT                   /note= "Transmembrane domain"
FT   Region          364. .375
FT                   /note= "lipoprotein lipid attachment site"
FT   Domain          431. .451
FT                   /note= "Transmembrane domain"
FT   Domain          474. .489
FT                   /note= "Transmembrane domain"
FT   Region          525. .531
FT                   /note= "N-myristoylation site"
FT   Domain          560. .535
FT                   /note= "Transmembrane domain"
FT   Region          627. .633
FT                   /note= "N-myristoylation site"
FT   Region          631. .637
FT                   /note= "N-myristoylation site"
FT   Region          640. .646
FT                   /note= "N-myristoylation site"
FT   Region          661. .667
FT                   /note= "N-myristoylation site"
XX
PN   WO200218608-A2.
XX
PD   07-MAR-2002.
XX
PF   10-JUL-2001; 2001WO-US021635.
XX
PR   29-AUG-2000; 2000US-0228914P.
PR   11-JAN-2001; 2001US-00759056.
PR   10-JUL-2001; 2001US-00901812.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Tice D,  Pennica D,  Polakis P,  Szeto W;
XX
DR   WPI; 2002-292202/33.
DR   N-PSDB; ABK47278.
XX
PT   Selectively enhancing the expression of a protein in a tumor cell
PT   characterized by aberrant Wnt signaling, useful for enhancing the
PT   efficacy of treatment of cancers, comprises treating the tumor cell with
PT   a retinoid.
XX
PS   Example 1; Fig 2; 141pp; English.
XX
CC   This invention relates to a novel method for selective enhancement of the
CC   expression of a protein in a tumour cell characterised by aberrant Wnt
CC   signalling by treating the tumour cell with a retinoid. The method is
CC   useful for enhancing the efficacy of treatment of cancers characterised
CC   by aberrant Wnt signalling, and for identifying tumour antigens the
CC   expression of which is selectively enhanced by retinoid treatment. The
CC   method is also useful in the early detection of tumours for early
CC   intervention. The tumour antigens are useful as targets for cancer
CC   therapy, since selective enhancement of their expression by retinoid
CC   treatment relative to normal cells improves the efficacy and therapeutic
CC   index of cancer therapeutics directed against these antigens. Antibodies
CC   binding to the tumour antigens may be administered for the treatment of
CC   various disorders or conditions, including those characterised by
CC   overexpression and/or activation of the tumour antigens, where such
CC   conditions or disorders include benign or malignant tumours; leukaemias
CC   and lymphoid malignancies; neuronal, glial, astrocytal, hypothalamic and
CC   other glandular, macrophagal, epithelial, stromal and blastocoelic
CC   disorders. The present sequence represents the human Stra6 protein
CC   (PRO10282) which is selectively upregulated by retinoid using the method
CC   of the invention. The gene encoding the human Stra6 protein is located on
CC   human chromosome 15q23
XX
SQ   Sequence 667 AA;

  Query Match             65.5%;  Score 1110.5;  DB 5;  Length 667;
  Best Local Similarity   76.6%;  Pred. No. 2.4e-106;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |              | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                  |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                   :::  |     ||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667


RESULT 12
ABB05048
ID   ABB05048 standard; protein; 667 AA.
XX
AC   ABB05048;
XX
DT   25-MAR-2002  (first entry)
XX
DE   Human NOV8c protein SEQ ID NO:32.
XX
KW   Human; NOVX; cytostatic; antidiabetic; anorectic; antibacterial;
KW   fungicide; virucide; protozoacide; analgesic; antiparkinsonian;
KW   antiasthmatic; hypotensive; osteopathic; antiinflammatory; antiulcer;
KW   neuroprotective; cardiant; antiallergic; antidepressant; nootropic;
KW   anticonvulsant; neuroleptic; gene therapy; vaccine; immune disease;
KW   developmental disease; taste and scent detectability disorder; infection;
KW   Burkitt's lymphoma; signal transduction pathway disorder; pain; cancer;
KW   retinal disease; feeding disorder; asthma; Parkinson's disease; ulcer;
KW   noninsulin-dependent diabetes mellitus; acute heart failure; hypotension;
KW   hypertension; urinary retention; osteoporosis; Crohn's disease; allergy;
KW   multiple sclerosis; angina pectoris; myocardial infarction; delirium;
KW   benign prostatic hypertrophy; manic depression; dementia; dyskinesia;
KW   severe metal retardation; Huntington's disease; chromosome 15;
KW   Gilles de la Tourette syndrome.
XX
OS   Homo sapiens.
XX
PN   WO200190155-A2.
```

```
XX
PD   29-NOV-2001.
XX
PF   24-MAY-2001; 2001WO-US017073.
XX
PR   24-MAY-2000; 2000US-0206679P.
PR   24-MAY-2000; 2000US-0206688P.
PR   24-MAY-2000; 2000US-0206829P.
PR   30-MAY-2000; 2000US-0207748P.
PR   30-MAY-2000; 2000US-0207798P.
PR   31-MAY-2000; 2000US-0208263P.
PR   02-JUN-2000; 2000US-0208831P.
PR   05-JUN-2000; 2000US-0209451P.
PR   07-JUN-2000; 2000US-0210060P.
PR   20-JUL-2000; 2000US-0219507P.
PR   26-JUL-2000; 2000US-0221337P.
PR   31-JUL-2000; 2000US-0221927P.
PR   19-JAN-2001; 2001US-0263135P.
PR   24-JAN-2001; 2001US-0263688P.
PR   24-JAN-2001; 2001US-0263694P.
PR   23-MAY-2001; 2001US-00863776.
XX
PA   (CURA-) CURAGEN CORP.
XX
PI   Spytek KA,  Majumder K,  Tchernev VT,  Mishra V,  Padigaru M;
PI   Spaderna SK,  Shenoy S,  Rastelli L,  Li L,  Taupier RJ,  Gangolli E;
XX
DR   WPI; 2002-106174/14.
DR   N-PSDB; ABA92669.
XX
PT   Novel polypeptide, useful for treating pain, cancer, urinary retention,
PT   osteoporosis, Crohn's disease, diabetes, acute heart failure, dementia,
PT   asthma, ulcer, allergy and Huntington's disease, comprises isolated
PT   polypeptide NOVX.
XX
PS   Claim 1; Page 106; 266pp; English.
XX
CC   The present invention describes human NOVX proteins (NOV1 to NOV9). NOVX
CC   proteins (I) have cytostatic, antidiabetic, anorectic, antibacterial,
CC   fungicide, virucide, protozoacide, analgesic, antiparkinsonian,
CC   antiasthmatic, hypotensive, osteopathic, antiinflammatory, antiulcer,
CC   neuroprotective, cardiant, antiallergic, antidepressant, nootropic,
CC   anticonvulsant and neuroleptic activities. (I) and polynucleotides (II)
CC   can be used in gene therapy and vaccine production. (I) and (II) can be
CC   used for treating or preventing a NOVX-associated disorder such as
CC   cardiomyopathy, atherosclerosis and diabetes in a human, where the
CC   disorder is related to cell signal processing and metabolic path way
CC   modulation, in a subject, preferably human. (I) and (II) can be used for
CC   diagnosing, preventing or treating developmental diseases, immune
CC   diseases, taste and scent detectability disorder, Burkitt's lymphoma,
CC   signal transduction pathway disorders, retinal diseases including those
CC   involving photoreception, cell growth rate disorders, feeding disorders,
CC   noninsulin-dependent diabetes mellitus, infections, pain, cancer, asthma,
CC   Parkinson's disease, acute heart failure, hypotension, hypertension,
CC   urinary retention, osteoporosis, Crohn's disease, multiple sclerosis,
CC   Albright Hereditary Osteodystrophy, angina pectoris, ulcers, myocardial
CC   infarction, allergies, benign prostatic hypertrophy, manic depression,
CC   delirium, dementia, severe metal retardation and dyskinesias, such as
CC   Huntington's disease or Gilles de la Tourette syndrome. The present
CC   sequence represents the human NOV8c protein from the present invention.
CC   Human NOV2a is isolated to chromosome 15
XX
SQ   Sequence 667 AA;

  Query Match             65.5%;  Score 1110.5;  DB 5;  Length 667;
  Best Local Similarity   76.6%;  Pred. No. 2.4e-106;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD-------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |   | : |               | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                                                                          |
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                  :::  |      |||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667
```

RESULT 13
AAO19413
ID   AAO19413 standard; protein; 667 AA.
XX
AC   AAO19413;
XX
DT   10-DEC-2002 (first entry)
XX
DE   Human molecule for disease detection and treatment protein #16.
XX
KW   Human; molecule for disease detection and treatment; MDDT; gene therapy;
KW   cytostatic; antiarteriosclerotic; hepatotropic; anti-HIV; antiallergic;
KW   antiinflammatory; antiasthmatic; cerebroprotective; nootropic;
KW   neuroprotective; antiparkinsonian; cardiant; antianginal.
XX
OS   Homo sapiens.
XX
PN   WO200270709-A2.
XX
PD   12-SEP-2002.
XX
PF   08-FEB-2002; 2002WO-US003709.
XX
PR   09-FEB-2001; 2001US-0268117P.
PR   15-FEB-2001; 2001US-0269618P.
PR   23-FEB-2001; 2001US-0271118P.
PR   07-MAR-2001; 2001US-0274486P.
PR   09-MAR-2001; 2001US-0274436P.
PR   28-NOV-2001; 2001US-0334229P.
PR   01-FEB-2002; 2002US-0353284P.
XX
PA   (INCY-) INCYTE GENOMICS INC.
XX
PI   Lal PG, Baughn MR, Yao MG, Walia NK, Elliot VS, Xu Y;
PI   Honchell CD, Yue H, Ding L, Gietzen KJ, Ison CH, Lu DAM;
PI   Hafalia AJA, Ghandi AR, Thangavelu K, Sanjanwala MM, Tang YT;
PI   Ramkumar J, Griffin JA, Swarnaker A, Azimzai Y, Sapperstein SK;
PI   Burford N, Lee EA, Lu Y, Tran UK, Marquis JP;
XX
DR   WPI; 2002-713453/77.
DR   N-PSDB; AAL49942.
XX
PT   New human molecules for disease detection and treatment (MDDT), useful
PT   for diagnosing, treating and preventing diseases or conditions associated
PT   with the aberrant MDDT expression, e.g. cancer, AIDS, asthma, diabetes,
PT   hepatitis.
XX
PS   Claim 1; Page 148-150; 177pp; English.
XX
CC   The present invention relates to human proteins and coding sequences of
CC   molecules for disease detection and treatment MDDT. The sequences can be
CC   used in the treatment of diseases associated with the decreased
CC   expression or overexpression of MDDT, such as cell proliferative (cancer,

CC atherosclerosis, hepatitis), autoimmune/inflammatory (e.g. AIDS,
CC allergies, Addison's disease, asthma), developmental (dwarfism, renal
CC tubular acidosis), neurological (e.g. stroke, Parkinson's disease,
CC epilepsy) and cardiovascular (congestive heart failure, myocardial
CC infarction, angina pectoris) disorders. The present sequence is a protein
CC of the invention
XX
SQ Sequence 667 AA;

Query Match 65.5%; Score 1110.5; DB 5; Length 667;
Best Local Similarity 76.6%; Pred. No. 2.4e-106;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

```
Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |              | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              |||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                 :::  |      |||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667
```

RESULT 14
ABU80778
ID ABU80778 standard; protein; 667 AA.
XX
AC ABU80778;
XX
DT 23-JUN-2003 (first entry)
XX
DE Human PRO polypeptide #40.
XX
KW Human; PRO polypeptide; secreted and transmembrane protein;
KW anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
XX
OS Homo sapiens.
XX
PN US2003036635-A1.
XX
PD 20-FEB-2003.
XX
PF 28-AUG-2002; 2002US-00230163.
XX
PR 25-JUL-2000; 2000US-0220638P.
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-342045/32.
DR N-PSDB; ACA66880.
XX
PT One hundred and twenty two nucleic acids encoding PRO polypeptides,
PT useful for the manufacture of a medicament for diagnosing or treating
PT tumor.
XX
PS Claim 11; Fig 80; 314pp; English.
XX
CC The present invention relates to the isolation of novel human PRO
CC polypeptides, and the polynucleotide sequences encoding them. The PRO
CC polypeptides are secreted and transmembrane proteins. The PRO
CC polypeptides and polynucleotides are useful for preparing a medicament
CC useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are
CC useful in diagnostic assays for PRO, by detecting its expression in
CC specific cells, tissues or serum, and for affinity purification of PRO
CC from recombinant cell culture or natural sources. ABU80739-ABU80860
CC represent the human PRO polypeptides of the invention. Note: The sequence
CC data for this patent was obtained in electronic format directly from the
CC USPTO web site at seqdata.uspto.gov/psipsDIDEntry.html
XX
SQ Sequence 667 AA;

Query Match 65.5%; Score 1110.5; DB 6; Length 667;
Best Local Similarity 76.6%; Pred. No. 2.4e-106;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

```
Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |              | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              |||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                 :::  |      |||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667
```

RESULT 15
ABO33744
ID ABO33744 standard; protein; 667 AA.
XX
AC ABO33744;
XX
DT 17-SEP-2003 (first entry)
XX
DE Novel human secreted and transmembrane protein PRO10282.
XX
KW Human; secreted and transmembrane protein; PRO; cytostatic;
KW antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha;
KW chondrocyte stimulator; pericyte stimulator; fibroblast modulator;
KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour;
KW colon tumour; breast tumour; prostate tumour; rectal tumour;
KW liver tumour; bone disorder; cartilage disorder; sports injury;
KW arthritis; wound.
XX
OS Homo sapiens.
XX
PN US2003045687-A1.
XX
PD 06-MAR-2003.
XX
PF 12-AUG-2002; 2002US-00218631.

XX
PR 01-JUN-2001; 2001WO-US017800.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-APR-2002; 2002US-00119480.
XX
PA (GETH) GENENTECH INC.
XX
PI Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WI;
XX
DR WPI; 2003-512315/48.
DR N-PSDB; ACD68632.
XX
PT New genes, and its encoded secreted and transmembrane polypeptides,
PT useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or
PT pericyte proliferation, especially for treating lung tumors, arthritis or
PT wounds in a mammal.
XX
PS Claim 11; Fig 80; 314pp; English.
XX
CC The invention describes an isolated nucleic acid molecule comprising a
CC sequence with at least 80% identity to: (a) a nucleotide encoding any of
CC 122 PRO (secreted and transmembrane) polypeptides whose sequences are
CC fully defined in the specification; or (b) any of 122 nucleotide
CC sequences having e.g. 4834, 2504 or 1759 bp fully defined in the
CC specification; or the full length coding sequence of any these 122
CC nucleotide sequences. The PRO polypeptides or polynucleotides are useful
CC as pharmaceuticals, diagnostics, biosensors or bioreactors. These are
CC particularly useful for detecting tumours (e.g. lung tumour, colon
CC tumour, breast tumour, prostate tumour, rectal tumour, or liver tumour)
CC in a mammal, for stimulating the release of TNF-alpha from human blood,
CC for stimulating the proliferation or differentiation of chondrocyte
CC cells, for stimulating proliferation of pericyte cells, or for modulating
CC normal human dermal fibroblast proliferation. The PRO nucleic acid or
CC polypeptide is also useful for treating tumours or various bone and/or
CC cartilage disorders (e.g. sports injuries or arthritis), or wounds. The
CC PRO polypeptides are useful in drug screening, particularly as targets
CC for therapeutic intervention in these diseases, and in the diagnostic
CC determination of the presence of these diseases. The PRO polypeptides are
CC also useful as molecular weight markers, or for chromosome
CC identification. The PRO genes are useful as hybridisation probes, or for
CC screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may
CC also be used in gene therapy, particularly for replacing a defective
CC gene. This is the amino acid sequence of a novel human secreted and
CC transmembrane PRO polypeptide
XX
SQ Sequence 667 AA;

Query Match 65.5%; Score 1110.5; DB 6; Length 667;
Best Local Similarity 76.6%; Pred. No. 2.4e-106;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

```
Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD----------GQFSWNLFS 42
              |||||||||||||||||||||||      |  | : |             | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                  |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC---------- 149
              |||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                  :::  |      ||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
```

Db 665 AQP 667

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Job time : 146.513 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 13:30:00 ; Search time 38.4542 Seconds
(without alignments)
630.905 Million cell updates/sec

Title: US-09-816-653A-4
Perfect score: 1695
Sequence: 1 CYISALVLSCLLTFLVLMRS.....APPTWLWESQQGFWRKKLVG 325

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	440	26.0	88	4	US-09-205-258-274	Sequence 274, App
2	98.5	5.8	157	4	US-09-252-991A-30836	Sequence 30836, A
3	94.5	5.6	726	4	US-09-252-991A-18271	Sequence 18271, A
4	93.5	5.5	422	4	US-09-252-991A-19452	Sequence 19452, A
5	93	5.5	2016	3	US-09-634-920-4	Sequence 4, Appli
6	93	5.5	2016	4	US-09-514-907A-2	Sequence 2, Appli
7	93	5.5	2016	4	US-09-896-994-2	Sequence 2, Appli
8	93	5.5	2016	4	US-09-840-125-4	Sequence 4, Appli
9	92	5.4	1272	4	US-09-949-016-7472	Sequence 7472, Ap
10	92	5.4	2146	4	US-09-949-016-6947	Sequence 6947, Ap
11	90.5	5.3	557	4	US-09-902-540-12884	Sequence 12884, A
12	90.5	5.3	1241	4	US-08-714-741-34	Sequence 34, Appl
13	90	5.3	327	4	US-09-252-991A-29468	Sequence 29468, A
14	89.5	5.3	275	4	US-09-252-991A-16752	Sequence 16752, A
15	89.5	5.3	434	4	US-09-252-991A-30855	Sequence 30855, A
16	89	5.3	249	4	US-09-602-777A-344	Sequence 344, App
17	88.5	5.2	501	4	US-09-252-991A-32497	Sequence 32497, A
18	87	5.1	618	3	US-08-866-381A-6	Sequence 6, Appli
19	87	5.1	621	1	US-08-208-887A-49	Sequence 49, Appl
20	87	5.1	621	3	US-09-280-598-18	Sequence 18, Appl
21	87	5.1	621	4	US-08-945-771-4	Sequence 4, Appli
22	86.5	5.1	465	4	US-09-496-239A-18	Sequence 18, Appl
23	86	5.1	597	4	US-09-252-991A-24252	Sequence 24252, A
24	85.5	5.0	395	4	US-09-489-039A-12123	Sequence 12123, A
25	85	5.0	809	4	US-09-252-991A-31759	Sequence 31759, A
26	84.5	5.0	299	4	US-09-393-634-41	Sequence 41, Appl
27	84.5	5.0	738	4	US-09-949-016-10957	Sequence 10957, A
28	84	5.0	484	4	US-09-252-991A-32299	Sequence 32299, A
29	84	5.0	529	4	US-09-489-039A-7581	Sequence 7581, Ap
30	84	5.0	595	4	US-09-252-991A-17434	Sequence 17434, A
31	84	5.0	1395	4	US-09-949-016-7109	Sequence 7109, Ap
32	83.5	4.9	922	4	US-09-569-611C-41	Sequence 41, Appl
33	83.5	4.9	971	4	US-09-868-572A-1	Sequence 1, Appli
34	83	4.9	526	4	US-09-438-185A-37	Sequence 37, Appl
35	83	4.9	539	3	US-09-036-987A-11	Sequence 11, Appl
36	83	4.9	539	3	US-09-370-700-11	Sequence 11, Appl
37	83	4.9	539	4	US-09-603-207-11	Sequence 11, Appl
38	83	4.9	1122	4	US-09-252-991A-22843	Sequence 22843, A
39	83	4.9	1495	3	US-08-462-467B-12	Sequence 12, Appl
40	82.5	4.9	216	4	US-09-134-000C-4728	Sequence 4728, Ap
41	82.5	4.9	344	4	US-09-252-991A-24536	Sequence 24536, A
42	82.5	4.9	1024	4	US-09-562-737-84	Sequence 84, Appl
43	82.5	4.9	2972	4	US-08-469-260A-387	Sequence 387, App
44	82.5	4.9	2972	4	US-08-488-446-387	Sequence 387, App
45	82.5	4.9	2972	4	US-08-467-344A-387	Sequence 387, App

ALIGNMENTS

RESULT 1
US-09-205-258-274
; Sequence 274, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: PZ007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06

; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 274
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (53)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (88)
; OTHER INFORMATION: Xaa equals stop translation
US-09-205-258-274

Query Match 26.0%; Score 440; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.3e-39;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy        180 MTAFCSLLLQAQSLLPRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWG 239
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MTAFCSLLLQAQSLLPRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWG 60

Qy        240 LAYTLLHNPTLQVFRKTALLGANGAQP 266
              ||||||||||||||||||||||||||
Db         61 LAYTLLHNPTLQVFRKTALLGANGAQP 87
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RESULT 2
US-09-252-991A-30836
; Sequence 30836, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30836
; LENGTH: 157
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30836

Query Match 5.8%; Score 98.5; DB 4; Length 157;
Best Local Similarity 33.0%; Pred. No. 0.015;
Matches 30; Conservative 6; Mismatches 26; Indels 29; Gaps 3;

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Qy        195 PRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFR 254
              |      :|  ||          : : | | |||||| |||||   |
Db          2 PAARRGCRDRARP----------RPRRSPAPGARPGARRGRARHSTA------------ 38

Qy        255 KTALLGANGAQPCSSL--PGSPPSITPAMQP 283
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Db         39 ----TGRRPARPAATLAGPGSPPGCRPAAIP 65
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RESULT 3
US-09-252-991A-18271
; Sequence 18271, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18271
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18271

Query Match 5.6%; Score 94.5; DB 4; Length 726;
Best Local Similarity 31.7%; Pred. No. 0.31;
Matches 33; Conservative 10; Mismatches 44; Indels 17; Gaps 5;

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Qy        194 LPR--TMAAPQDSLRPGEEDEG--MQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPT 249
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Db        273 LPRQGTAVLHRDPGRPGDPDGGDRLRLLPDPPAQADQSHPGDPHGRG--GRRFP------ 324

Qy        250 LQVFRKTALLGANGAQPCSSLPGSPPSITPAMQPAGPPDHXGXV 293
                  |:  ||   | ||   ||   | : | : |  |  | | |
Db        325 ----RRVPLLPRAGLQPGGQLPERQPGL-PRLDPGWPAVHQGPV 363
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RESULT 4
US-09-252-991A-19452
; Sequence 19452, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

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;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 19452
;   LENGTH: 422
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19452

  Query Match             5.5%;  Score 93.5;  DB 4;  Length 422;
  Best Local Similarity   23.8%;  Pred. No. 0.19;
  Matches   48;  Conservative   14;  Mismatches   73;  Indels   67;  Gaps   10;

Qy        135 LFPLNVLVGAMXXXCSPSIAIRHPTPGYYTYRNFLKIEVSQSHP-AMTAFCSLLLQAQSL 193
              | ||   |  :   |   :    |  |              |: | :  || ||     ||
Db        129 LIPLGCFVPLVSILCHRRLRNAKPRSG------------QTAPDSQAAFLSL---RYSL 172

Qy        194 LPRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRG----------------RAR 237
                :  | |           |:   :|:    ||   |  ||                |
Db        173 ALKISATP----------GVDEYKTR----KGNMSGPLRGVFLTPGTPAPRKLVTSRRG 217

Qy        238 WGLAYTLLHNPTLQVFRKTALLGANGAQPCSSLPGSPPSITPAMQPAGPPDHXGXVEVCL 297
              | ||   |   : :   ::           |||  | :||:  ||  |   |     |
Db        218 NGNAY---HQSHISIHTASS----------HHLPGGAPCLTPSSTPAVSPTTIGSCTPCC 264

Qy        298 HWEPXXGSAPPTWLWESQQGFW 319
              |    ||  |||      | |
Db        265 -WMRKAGSCSPTW-----YGCW 280


RESULT 5
US-09-634-920-4
; Sequence 4, Application US/09634920
; Patent No. 6342357
; GENERAL INFORMATION:
;  APPLICANT:  Splawski, Igor
;  APPLICANT:  Keating, Mark T.
;  TITLE OF INVENTION:  ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
;  TITLE OF INVENTION:  SCN5A AND METHODS FOR DETECTING SAME
;  FILE REFERENCE:  2323-155
;  CURRENT APPLICATION NUMBER: US/09/634,920
;  CURRENT FILING DATE:  2000-08-09
;  PRIOR APPLICATION NUMBER:  60/190,057
;  PRIOR FILING DATE:  2000-03-17
;  PRIOR APPLICATION NUMBER:  60/147,488
;  PRIOR FILING DATE:  1999-08-09
;  NUMBER OF SEQ ID NOS:  4
;  SOFTWARE:  PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 2016
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-634-920-4

  Query Match             5.5%;  Score 93;  DB 3;  Length 2016;
  Best Local Similarity   23.8%;  Pred. No. 1.8;
  Matches   67;  Conservative   31;  Mismatches  113;  Indels   70;  Gaps   13;

Qy         35 QFSWNLFSVPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFW 94
              |  ||:|           ::|   :  || : :: |    ||    ||     |  |||
Db        778 QQGWNIFD---------SIIVILSLMELGLSRMSNL---SVLRSFRLLRVFKLAKSWPTL 825

Qy         95 ---------------LTLALAVILQNMAAHWV------FLETHDGHPQLTNR---RVLY 129
                            ||| ||:|:   |   :      : | |    | |      :
Db        826 NTLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFF 885

Qy        130 AATFLLFPLNVLVGAMXXXCSPSIAIRHPTPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQ 189
              |  ::|   :| |          : :   :          || : |  :   :  | :|||
Db        886 HAFLIIF--RILCGEWIETMWDCMEVSGQS---LCLLVFLLVMVIGNLVVLNLFLALLLS 940

Qy        190 AQSLLPRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLL-HNP 248
              : |           |:|   :||  |  ||   ::|:  |       |  |      || | |
Db        941 SFS---------ADNLTAPDEDREMNNLQL--ALARIQRGLRFVKRTTWDFCCGLLRHRP 989

Qy        249 TLQVFRKTALLGANGAQP-CSSLPGSPPSITPAMQPAGPPD 288
                  :| | | | | | | : | |||          ||:
Db        990 -----QKPAALAAQGQLPSCIATPYSPP----------PPE 1015


RESULT 6
US-09-514-907A-2
; Sequence 2, Application US/09514907A
; Patent No. 6567705
;  GENERAL INFORMATION:
;       APPLICANT: Kenneth B. Stokes
;                  Jos,e Morissette
;       TITLE OF INVENTION: SYSTEMS FOR ENHANCING CARDIAC SIGNAL
;                           SENSING BY CARDIAC PACEMAKERS THROUGH
;                           GENETIC TREATMENT
;       NUMBER OF SEQUENCES: 12
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6567705ris LLP
;            STREET: One Liberty Place - 46th Floor
;            CITY: Philadelphia
;            STATE: PA
;            COUNTRY: U.S.A.
;            ZIP: 19103
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: WordPerfect 6.1
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/09/514,907A
;            FILING DATE: 08-Feb-2000
;            CLASSIFICATION: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Paul K. Legaard
;            REGISTRATION NUMBER: 38,534
;            REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (215) 568-3100
;            TELEFAX: (215) 568-3439
;  INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2016 amino acids
;            TYPE: amino acid
;            STRANDEDNESS: single
;            TOPOLOGY: unknown
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-514-907A-2

  Query Match             5.5%;  Score 93;  DB 4;  Length 2016;
  Best Local Similarity   23.8%;  Pred. No. 1.8;
  Matches   67;  Conservative   31;  Mismatches  113;  Indels   70;  Gaps   13;

Qy         35 QFSWNLFSVPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFW 94
              |  ||:|           ::|   :  || : :: |    ||    ||     |  |||
Db        778 QQGWNIFD---------SIIVILSLMELGLSRMSNL---SVLRSFRLLRVFKLAKSWPTL 825

Qy         95 ---------------LTLALAVILQNMAAHWV------FLETHDGHPQLTNR---RVLY 129
                            ||| ||:|:   |   :      : | |    | |      :
Db        826 NTLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFF 885

Qy        130 AATFLLFPLNVLVGAMXXXCSPSIAIRHPTPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQ 189
              |  ::|   :| |          : :   :          || : |  :   :  | :|||
Db        886 HAFLIIF--RILCGEWIETMWDCMEVSGQS---LCLLVFLLVMVIGNLVVLNLFLALLLS 940

Qy        190 AQSLLPRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLL-HNP 248
              : |           |:|   :||  |  ||   ::|:  |       |  |      || | |
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Db        941 SFS---------ADNLTAPDEDREMNNLQL--ALARIQRGLRFVKRTTWDFCCGLLRHRP 989

Qy        249 TLQVFRKTALLGANGAQP-CSSLPGSPPSITPAMQPAGPPD 288
                  :| | | | |  | | : | |||          ||:
Db        990 -----QKPAALAAQGQLPSCIATPYSPP----------PPE 1015


RESULT 7
US-09-896-994-2
; Sequence 2, Application US/09896994
; Patent No. 6665563
;   GENERAL INFORMATION:
;        APPLICANT: Ken Stokes
;                   Jos e Morissette
;        TITLE OF INVENTION: SYSTEMS AND METHODS FOR ENHANCING CARDIAC
;                            SIGNAL SENSING BY CARDIAC PACEMAKERS THROUGH GENETIC TREATM
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz and No. 6665563ris
;             STREET: One Liberty Place - 46th Floor
;             CITY: Philadelphia
;             STATE: PA
;             COUNTRY: U.S.A.
;             ZIP: 19103
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: WordPerfect 6.1
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/896,994
;             FILING DATE: 02-Jul-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/514,907
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Paul K. Legaard
;             REGISTRATION NUMBER: 38,534
;             REFERENCE/DOCKET NUMBER: MEDT-0029/P-3586
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (215) 568-3100
;             TELEFAX: (215) 568-3439
;   INFORMATION FOR SEQ ID NO: 2:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 2016 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: unknown
;        SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-896-994-2

  Query Match             5.5%;  Score 93;  DB 4;  Length 2016;
  Best Local Similarity   23.8%;  Pred. No. 1.8;
  Matches   67;  Conservative   31;  Mismatches  113;  Indels   70;  Gaps   13;

Qy         35 QFSWNLFSVPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFW 94
              |  ||:|           ::|   :  || : :: |    ||    ||    |  |||
Db        778 QQGWNIFD---------SIIVILSLMELGLSRMSNL---SVLRSFRLLRVFKLAKSWPTL 825

Qy         95 ----------------LTLALAVILQNMAAHWV------FLETHDGHPQLTNR---RVLY 129
                            ||| ||:|:   |   :      : |  |    |  |      :
Db        826 NTLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFF 885

Qy        130 AATFLLFPLNVLVGAMXXXCSPSIAIRHPTPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQ 189
               |  ::|   :| |          : :   :        || : |  :   :  | :|||
Db        886 HAFLIIF--RILCGEWIETMWDCMEVSGQS---LCLLVFLLVMVIGNLVVLNLFLALLLS 940

Qy        190 AQSLLPRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLL-HNP 248
              : |          |:|   :||  |  ||   ::|:  |       |  |      || | |
Db        941 SFS---------ADNLTAPDEDREMNNLQL--ALARIQRGLRFVKRTTWDFCCGLLRHRP 989

Qy        249 TLQVFRKTALLGANGAQP-CSSLPGSPPSITPAMQPAGPPD 288
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                  :| | | | |  | | : | |||          ||:
Db        990 -----QKPAALAAQGQLPSCIATPYSPP----------PPE 1015


RESULT 8
US-09-840-125-4
; Sequence 4, Application US/09840125
; Patent No. 6787309
; GENERAL INFORMATION:
;  APPLICANT: Splawski, Igor
;  APPLICANT:  Keating, Mark T.
;  TITLE OF INVENTION: ALTERATIONS IN THE LONG QT SYNDROME GENES KVLQT1 AND
;  TITLE OF INVENTION:  SCN5A AND METHODS FOR DETECTING SAME
;  FILE REFERENCE: 2323-155
;  CURRENT APPLICATION NUMBER: US/09/840,125
;  CURRENT FILING DATE:  2001-04-24
;  PRIOR APPLICATION NUMBER: 09/634,920
;  PRIOR FILING DATE: 2000-08-09
;  PRIOR APPLICATION NUMBER: 60/147,488
;  PRIOR FILING DATE: 1999-08-09
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 2016
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-840-125-4

  Query Match             5.5%;  Score 93;  DB 4;  Length 2016;
  Best Local Similarity   23.8%;  Pred. No. 1.8;
  Matches   67;  Conservative   31;  Mismatches  113;  Indels   70;  Gaps   13;

Qy         35 QFSWNLFSVPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFW 94
              |  ||:|           ::|   :  || : :: |    ||    ||    |  |||
Db        778 QQGWNIFD---------SIIVILSLMELGLSRMSNL---SVLRSFRLLRVFKLAKSWPTL 825

Qy         95 ----------------LTLALAVILQNMAAHWV------FLETHDGHPQLTNR---RVLY 129
                            ||| ||:|:   |   :      : |  |    |  |      :
Db        826 NTLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFF 885

Qy        130 AATFLLFPLNVLVGAMXXXCSPSIAIRHPTPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQ 189
               |  ::|   :| |          : :   :        || : |  :   :  | :|||
Db        886 HAFLIIF--RILCGEWIETMWDCMEVSGQS---LCLLVFLLVMVIGNLVVLNLFLALLLS 940

Qy        190 AQSLLPRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLL-HNP 248
              : |          |:|   :||  |  ||   ::|:  |       |  |      || | |
Db        941 SFS---------ADNLTAPDEDREMNNLQL--ALARIQRGLRFVKRTTWDFCCGLLRHRP 989

Qy        249 TLQVFRKTALLGANGAQP-CSSLPGSPPSITPAMQPAGPPD 288
                  :| | | | |  | | : | |||          ||:
Db        990 -----QKPAALAAQGQLPSCIATPYSPP----------PPE 1015


RESULT 9
US-09-949-016-7472
; Sequence 7472, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 7472
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;   LENGTH: 1272
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-7472

  Query Match              5.4%;  Score 92;  DB 4;  Length 1272;
  Best Local Similarity   25.3%;  Pred. No. 1.2;
  Matches   80;  Conservative   48;  Mismatches  126;  Indels   62;  Gaps   17;

Qy          3 ISALVLSCL---LTF------LVLMRSLVT---HRLGSGGSGD-----GQFSWNL--FSV 43
              :  ||   |:   ::|      |||:   ||    |    ||        | | |::  : |
Db        660 VDVLVSICVVFAMSFVPASFTLVLIEERVTRAKHLQLMGGLSPTLYWLGNFLWDMCNYLV 719

Qy         44 PLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLL-------FFRSLESSWPFWLT 96
              |  :  |  |  ||   ::    |  |:|: :|:| ::        || |: |:    ||
Db        720 PACIVVLIFLAFQQRA-YVAPANLPALLLLLLLYGWSITPLMYPASFFFSVPSTAYVVLT 778

Qy         97 -LALAVILQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVL-VGAMXXXCSPSIA 154
               : | : :    | :|     |   |  :|  :    ||:||   |  | :    : ::|
Db        779 CINLFIGINGSMATFVLELFSDQKLQEVSR--ILKQVFLIFPHFCLGRGLIDMVRNQAMA 836

Qy        155 IRHPTPGYYTYRNFLKIEVSQSH--------PAMTAFCSLLLQAQSLL---PRTMAAPQD 203
                  |   ::: |: ||   :        |    | :|||| :| |   || : |
Db        837 DAFERLGDRQFQSPLRWEVVGKNLLAMVIQGPLFLLF-TLLLQHRSQLLPQPRVRSLP-- 893

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPG----------AXRGRARWGLAYTLLHNPTLQVF 253
              |||||   : : :: : :||  |            ||:    :    |  |  : |
Db        894 --LLGEEDE--DVARERERVVQGATQGDVLVLRNLTKVYRGQRMPAVDRLCLGIPPGECF 949

Qy        254 RKTALLGANGAQPCSS 269
              ||| |||   |:
Db        950 ---GLLGVNGAGKTST 962


RESULT 10
US-09-949-016-6947
; Sequence 6947, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;  APPLICANT: VENTER, J. Craig et al.
;  TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;  FILE REFERENCE: CL001307
;  CURRENT APPLICATION NUMBER: US/09/949,016
;  CURRENT FILING DATE:  2000-04-14
;  PRIOR APPLICATION NUMBER: 60/241,755
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/237,768
;  PRIOR FILING DATE: 2000-10-03
;  PRIOR APPLICATION NUMBER: 60/231,498
;  PRIOR FILING DATE: 2000-09-08
;  NUMBER OF SEQ ID NOS: 207012
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6947
;   LENGTH: 2146
;   TYPE: PRT
;   ORGANISM: Human
US-09-949-016-6947

  Query Match              5.4%;  Score 92;  DB 4;  Length 2146;
  Best Local Similarity   25.3%;  Pred. No. 2.5;
  Matches   80;  Conservative   48;  Mismatches  126;  Indels   62;  Gaps   17;

Qy          3 ISALVLSCL---LTF------LVLMRSLVT---HRLGSGGSGD-----GQFSWNL--FSV 43
              :  ||   |:   ::|      |||:   ||    |    ||        | | |::  : |
Db       1534 VDVLVSICVVFAMSFVPASFTLVLIEERVTRAKHLQLMGGLSPTLYWLGNFLWDMCNYLV 1593

Qy         44 PLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLL-------FFRSLESSWPFWLT 96
              |  :  |  |  ||   ::    |  |:|: :|:| ::        || |: |:    ||
Db       1594 PACIVVLIFLAFQQRA-YVAPANLPALLLLLLLYGWSITPLMYPASFFFSVPSTAYVVLT 1652

Qy         97 -LALAVILQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVL-VGAMXXXCSPSIA 154
               : | : :    | :|     |   |  :|  :    ||:||   |  | :    : ::|
Db       1653 CINLFIGINGSMATFVLELFSDQKLQEVSR--ILKQVFLIFPHFCLGRGLIDMVRNQAMA 1710

Qy        155 IRHPTPGYYTYRNFLKIEVSQSH--------PAMTAFCSLLLQAQSLL---PRTMAAPQD 203
                  |   ::: |: ||   :        |    | :|||| :| |   || : |
Db       1711 DAFERLGDRQFQSPLRWEVVGKNLLAMVIQGPLFLLF-TLLLQHRSQLLPQPRVRSLP-- 1767

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPG----------AXRGRARWGLAYTLLHNPTLQVF 253
              |||||   : : :: : :||  |            ||:    :    |  |  : |
Db       1768 --LLGEEDE--DVARERERVVQGATQGDVLVLRNLTKVYRGQRMPAVDRLCLGIPPGECF 1823

Qy        254 RKTALLGANGAQPCSS 269
              ||| |||   |:
Db       1824 ---GLLGVNGAGKTST 1836


RESULT 11
US-09-902-540-12884
; Sequence 12884, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
;  APPLICANT: Goldman, Barry S.
;  APPLICANT:  Hinkle, Gregory J.
;  APPLICANT:  Slater, Steven C.
;  APPLICANT:  Wiegand, Roger C.
;  TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
;  FILE REFERENCE: 38-10(15849)B
;  CURRENT APPLICATION NUMBER: US/09/902,540
;  CURRENT FILING DATE:  2001-07-10
;  PRIOR APPLICATION NUMBER: 60/217,883
;  PRIOR FILING DATE: 2000-07-10
;  NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 12884
;   LENGTH: 557
;   TYPE: PRT
;   ORGANISM: Myxococcus xanthus
US-09-902-540-12884

  Query Match              5.3%;  Score 90.5;  DB 4;  Length 557;
  Best Local Similarity   30.9%;  Pred. No. 0.58;
  Matches   50;  Conservative   11;  Mismatches   52;  Indels   49;  Gaps   10;

Qy          5 ALVLSCLLTFLVLMRSLVTHRLGSGG-----SGDGQFSWNLFSVPLPLPPLAGLLVQQII 59
              |  |:  |  |  |  ||| .||  |      :| |      | | | ||     ||:
Db        242 AAQLATSLLLLAPMAMLVTWALGRAGRVRLSAGKG-----LSSRPFPLGRARGLV----- 291

Qy         60 FFLGTTAL--AFLVLMPVLHGRNLLFFRSLESSWP---FWLTLALAVILQNMAAHW--VF 112
                ||  ::  | |||:|:      :   ||: |:     | ||| |           ||  |
Db        292 --LGAVSMTAAVLVLLPL----GAILLTSLQRSFGAALTWETLTL--------THWAGVL 337

Qy        113 LETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXCSPSIA 154
              ||    |   | | || ||           ||    |   :|
Db        338 LEPRTLH--ATGRSVLLAA----------GAGVLVCGLGLA 366


RESULT 12
US-08-714-741-34
; Sequence 34, Application US/08714741
; Patent No. 6500613
;  GENERAL INFORMATION:
;    APPLICANT:  Briles, David E.
;    APPLICANT:  McDaniel, Larry S.
;    APPLICANT:  Swiatlo, Edwin
;    APPLICANT:  Yother, Janet
;    APPLICANT:  Crain, Marilyn J.
;    APPLICANT:  Hollingshead, Susan
;    APPLICANT:  Tart, Rebecca
;    APPLICANT:  Brooks-Walter, Alexis
;    TITLE OF INVENTION:  PNEUMOCOCCAL GENES, PORTIONS THEREOF,
;    TITLE OF INVENTION:  EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
;    TITLE OF INVENTION:  PORTIONS AND PRODUCTS
;    NUMBER OF SEQUENCES:  47
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Curtis, Morris & Safford, P.C.
```

```
;      STREET:  530 Fifth Avenue
;      CITY:  New York
;      STATE:  New York
;      COUNTRY:  U.S.
;      ZIP:  10036
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/714,741
;      FILING DATE:  16-SEP-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Frommer Esq., William S.
;      REGISTRATION NUMBER:  25,506
;      REFERENCE/DOCKET NUMBER:  454312-2460
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 840-3333
;      TELEFAX:  (212) 840-0712
;  INFORMATION FOR SEQ ID NO:  34:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1241 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  amino acid
US-08-714-741-34

  Query Match             5.3%;  Score 90.5;  DB 4;  Length 1241;
  Best Local Similarity   23.8%;  Pred. No. 1.7;
  Matches   80;  Conservative   37;  Mismatches  138;  Indels   81;  Gaps   14;

Qy          7 VLSCLLTFLVLMRSLVTHRL-GSGGSGDGQFSWNLFSVPLPLPPLAGLLVQQIIFF-LGT 64
              :|  ||  : |: :| ||||  |   | | :   |:|    |    |||    ::  |
Db        788 LLEGLLYSVALLEALATHRLEASPPRGLGLY---LYSTHRGLNASPGLLEASPLYSGLAL 844

Qy         65 TALAFLVLMPVLHGRNLLFF----------RSLESSWPFWLTLALAVILQNMAAHWVFLE 114
               ||| | |  :|   | | :            | :|    : |||| :|: :      ||
Db        845 AALAGLALAGLLEASNGLLYSVALGLALALEGLNASNGLNVALALAGLLEGLGLG--LLE 902

Qy        115 TH-----DGHPQLTNRRVLYAATFLLFPL--------NVLVGAMXXXCSPSIAIRHPTPG 161
              :      :|    :   ||:|:  |  |         || :|      ||:  |      |
Db        903 SERLYSLEGLASPASNLELYSASPALAGLTHRASNASNVALG----LASPTYRILELYSG 958

Qy        162 YYTYRNFLK-----IEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQDSLRPGEEDEGMQL 216
                  |    |       :|   :|   : : :|    : ||  |                |: |
Db        959 LGLYLEGLGLALAILEALATHRLYSLYSALAGLLEGLLYST-------------HRGLNL 1005

Qy        217 ---------------LQTKDSMAKGARPGAXRG-RARWGLAYTLLHNPTLQVFRKTALLG 260
                            |:  : : :|  | |  |  |  ||   | | |     |  |  |
Db       1006 YSGLLEASPALAALALEASNGLLEGLYPRASPGLYASPGLGLGLTHRPRALAPRALAPRG 1065

Qy        261 AN------------GAQPCSSLPGSPPSITP-AMQP 283
               |            |       |  :| :: | |: |
Db       1066 LNPRGLLYSPRALAGLGLPRGLASNPRALAPRALAP 1101


RESULT 13
US-09-252-991A-29468
; Sequence 29468, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER:  US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 29468
;   LENGTH:  327
;   TYPE:  PRT
;   ORGANISM:  Pseudomonas aeruginosa
US-09-252-991A-29468

  Query Match             5.3%;  Score 90;  DB 4;  Length 327;
  Best Local Similarity   21.9%;  Pred. No. 0.32;
  Matches   70;  Conservative   27;  Mismatches  126;  Indels   96;  Gaps   11;

Qy         28 SGGSGDGQFSWNLFSVPLPLPPLAGLLVQQ-----------IIFFLGTTALAFLV----- 71
              | |    ||        ||       ||   |           :  |||   |:||
Db         21 SSGGPTMQFFLRYAYAPLFWSGFIGLATWQVGYRQASHAWLVALFLGALGLSFLAERRLP 80

Qy         72 ------------LMPVLHGR-----NLL-------------FFRSLESSWPFWLTLALAV 101
                          |  |||       | |             |:     :|| || | ||:
Db         81 YQPRWNRPHADRLRDVLHASVNESLNALGILALPLLAGVLGFWPVWPQAWPLWLQLLLAI 140

Qy        102 ILQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXCSPSIAIRHPTPG 161
              :| ::     |   :|                : ||: |:              |: |
Db        141 VLADLGITLVHYASH--------------RSALLWRLH-------------AVHHSVQR 172

Qy        162 YYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQDSLRPGEEDEGMQLLQTKD 221
                | :  :|  :      |:     |||     :|:|:||            |:|||
Db        173 LYGFNGLMKHPLHLGLEALGGTLPLLLLG---VPQTVAALLAFA------IGIQLLLQHS 223

Qy        222 SMAKGARPGAXRGRARWGLAYTLLH---------NPTLQVFRKTALLGANGAQPCSSLPG 272
              ::    | |  |    |   : | |         |  |       |||    :|   |
Db        224 NV--DMRIGGLRHVFAWAPLHRLHHIRYGRAGDVNFALFFSVWDRLLGTALHRPDYRLDS 281

Qy        273 SPPSITPAMQPAGPPDHXG 291
              :   |    ||  | |: |
Db        282 TDMGI--GDQPDYPRDYAG 298


RESULT 14
US-09-252-991A-16752
; Sequence 16752, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER:  US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 16752
;   LENGTH:  275
;   TYPE:  PRT
;   ORGANISM:  Pseudomonas aeruginosa
US-09-252-991A-16752

  Query Match             5.3%;  Score 89.5;  DB 4;  Length 275;
  Best Local Similarity   25.9%;  Pred. No. 0.28;
  Matches   43;  Conservative   16;  Mismatches   58;  Indels   49;  Gaps    8;

Qy        168 FLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGA 227
              |:|    :| |  :|  |    | :: ||                    | ||  :
Db         51 FMKTNSVRSRPTPSAPSSTARAAPAVSPR------------------LAQTSTAWPSRV 91

Qy        228 RPGAXR-GRAR----WGLAYTLLHNPTLQVFRKTA------LLGANGAQPC-----SSLP 271
              | |: |   ||    |            :  |  |      :|||  :|||     |::|
Db         92 RAGSSRCASARAWRCW------------RASRSAAACCNCSVLGATCSQPCSPSSSSAVP 139

Qy        272 GSPPS-ITPAMQPAGPPDHXGXVEVCLHWEPXXGSAPPTWLWESQQ 316
              || ||   ||   || |     : :|    |      | |  | |::
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```
Db        140 GSRPSTAAPAQTNAGMPRARAMIALCEVAPPRAVRMPAT-RWASRR 184


RESULT 15
US-09-252-991A-30855
; Sequence 30855, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
;  APPLICANT:  Marc J. Rubenfield et al.
;  TITLE OF INVENTION:  NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
;  TITLE OF INVENTION:  AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
;  FILE REFERENCE:  107196.136
;  CURRENT APPLICATION NUMBER: US/09/252,991A
;  CURRENT FILING DATE:  1999-02-18
;  PRIOR APPLICATION NUMBER:  US 60/074,788
;  PRIOR FILING DATE:  1998-02-18
;  PRIOR APPLICATION NUMBER:  US 60/094,190
;  PRIOR FILING DATE:  1998-07-27
;  NUMBER OF SEQ ID NOS:  33142
; SEQ ID NO 30855
;   LENGTH: 434
;   TYPE: PRT
;   ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30855

  Query Match             5.3%;  Score 89.5;  DB 4;  Length 434;
  Best Local Similarity   25.7%;  Pred. No. 0.53;
  Matches   53;  Conservative   14;  Mismatches   80;  Indels   59;  Gaps   11;

Qy        104 QNMAAHWVF-LETHDGHPQ------LTNRRVLYAATFLLFPLNVLVGAMXXXCSPSIAIR 156
              |  |  |:  : |  || |      |   |:| |  |   ||   |
Db          9 QAPAGTWLLQVGTQRGHHQFQVFATLLRARLLGAEVFADVPLQHFV-------------- 54

Qy        157 HPTPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQDSLRPGEEDEGMQL 216
              |       :|   : :: |   |  |    |||   |        | |:  | :|     |
Db         55 HQA----VHRTADRRDLLQHRRAFAALFQRLLQRPGL-------PGDAAHPRQE-----L 98

Qy        217 LQTKDSMAKGARPGAXRGRAR---WGLAYTLLHNPTLQVFRKTALLGANGAQPCSSLPGS 273
              |   | |          |   :   ||: |          ||:     ||   |    |
Db         99 LLPMDGM-------GHRSLLKVIYWGIVY----------FRRLDRTVANARHPDYPAPAP 141

Qy        274 PPSITPAMQPAGPPDHX-GXVEVCLH 298
              ||: |  ||||   |  | :   ||
Db        142 FPSVRPG-QPAGRAQHALGGIAHRLH 166


Search completed: February  8, 2005, 13:42:12
Job time : 40.4542 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 13:32:20 ; Search time 108.54 Seconds
(without alignments)
975.246 Million cell updates/sec

Title: US-09-816-653A-4
Perfect score: 1695
Sequence: 1 CYISALVLSCLLTFLVLMRS.....APPTWLWESQQGFWRKKLVG 325

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 1373511

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1679	99.1	325	10	US-09-816-653A-4	Sequence 4, Appli
2	1110.5	65.5	560	10	US-09-863-776-69	Sequence 69, Appl
3	1110.5	65.5	599	15	US-10-104-047-2306	Sequence 2306, Ap
4	1110.5	65.5	667	9	US-09-759-056-2	Sequence 2, Appli
5	1110.5	65.5	667	9	US-09-901-812-2	Sequence 2, Appli
6	1110.5	65.5	667	10	US-09-863-776-32	Sequence 32, Appl
7	1110.5	65.5	667	10	US-09-863-776-67	Sequence 67, Appl
8	1110.5	65.5	667	14	US-10-227-884-80	Sequence 80, Appl
9	1110.5	65.5	667	14	US-10-230-163-80	Sequence 80, Appl
10	1110.5	65.5	667	14	US-10-230-338-80	Sequence 80, Appl
11	1110.5	65.5	667	14	US-10-218-631-80	Sequence 80, Appl
12	1110.5	65.5	667	14	US-10-230-414-80	Sequence 80, Appl
13	1110.5	65.5	667	14	US-10-232-224-80	Sequence 80, Appl
14	1110.5	65.5	667	14	US-10-216-159A-80	Sequence 80, Appl
15	1110.5	65.5	667	14	US-10-218-849-80	Sequence 80, Appl
16	1110.5	65.5	667	14	US-10-227-873-80	Sequence 80, Appl
17	1110.5	65.5	667	14	US-10-227-883-80	Sequence 80, Appl
18	1110.5	65.5	667	14	US-10-219-076-80	Sequence 80, Appl
19	1110.5	65.5	667	14	US-10-230-434-80	Sequence 80, Appl
20	1110.5	65.5	667	14	US-10-219-003-80	Sequence 80, Appl
21	1110.5	65.5	667	14	US-10-219-075-80	Sequence 80, Appl
22	1110.5	65.5	667	14	US-10-219-464-80	Sequence 80, Appl
23	1110.5	65.5	667	14	US-10-219-466-80	Sequence 80, Appl
24	1110.5	65.5	667	14	US-10-219-479-80	Sequence 80, Appl
25	1110.5	65.5	667	14	US-10-219-481-80	Sequence 80, Appl
26	1110.5	65.5	667	14	US-10-230-260-80	Sequence 80, Appl
27	1110.5	65.5	667	14	US-10-232-231-80	Sequence 80, Appl
28	1110.5	65.5	667	14	US-10-232-233-80	Sequence 80, Appl
29	1110.5	65.5	667	14	US-10-216-165-80	Sequence 80, Appl
30	1110.5	65.5	667	14	US-10-218-956-80	Sequence 80, Appl
31	1110.5	65.5	667	14	US-10-219-468-80	Sequence 80, Appl
32	1110.5	65.5	667	14	US-10-219-478-80	Sequence 80, Appl
33	1110.5	65.5	667	14	US-10-219-536-80	Sequence 80, Appl
34	1110.5	65.5	667	14	US-10-233-205-80	Sequence 80, Appl
35	1110.5	65.5	667	14	US-10-219-072-80	Sequence 80, Appl
36	1110.5	65.5	667	14	US-10-219-470-80	Sequence 80, Appl
37	1110.5	65.5	667	14	US-10-219-474-80	Sequence 80, Appl
38	1110.5	65.5	667	14	US-10-219-524-80	Sequence 80, Appl
39	1110.5	65.5	667	14	US-10-219-528-80	Sequence 80, Appl
40	1110.5	65.5	667	14	US-10-227-880-80	Sequence 80, Appl
41	1110.5	65.5	667	14	US-10-227-881-80	Sequence 80, Appl
42	1110.5	65.5	667	14	US-10-227-882-80	Sequence 80, Appl
43	1110.5	65.5	667	14	US-10-230-436-80	Sequence 80, Appl
44	1110.5	65.5	667	14	US-10-232-223-80	Sequence 80, Appl
45	1110.5	65.5	667	14	US-10-232-225-80	Sequence 80, Appl

ALIGNMENTS

RESULT 1
US-09-816-653A-4
; Sequence 4, Application US/09816653A
; Publication No. US20030021788A1
; GENERAL INFORMATION:
; APPLICANT: Rastelli, Luca
; APPLICANT: Pennica, Diane
; TITLE OF INVENTION: NOVEL HUMAN STRA6-LIKE PROTEIN AND NUCLEIC ACIDS ENCODING THE SA
; FILE REFERENCE: 10716/57
; CURRENT APPLICATION NUMBER: US/09/816,653A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/191,532
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 325
; TYPE: PRT
; ORGANISM: Homo sapiens hSTRA6 polypeptide fragment, carboxy terminus
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (146)..(148)
; OTHER INFORMATION: Xaa represents any amino acid, other, or unkown
; NAME/KEY: MISC_FEATURE
; LOCATION: (232)..(232)
; OTHER INFORMATION: Xaa represents any amino acid, other, or unkown
; NAME/KEY: MISC_FEATURE
; LOCATION: (290)..(290)
; OTHER INFORMATION: Xaa represents any amino acid, other, or unkown
; NAME/KEY: MISC_FEATURE
; LOCATION: (292)..(292)
; OTHER INFORMATION: Xaa represents any amino acid, other, or unkown
; NAME/KEY: MISC_FEATURE
; LOCATION: (302)..(302)
; OTHER INFORMATION: Xaa represents any amino acid, other, or unkown
; NAME/KEY: MISC_FEATURE

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;   LOCATION: (303)..(303)
;   OTHER INFORMATION: Xaa represents any amino acid, other, or unkown
US-09-816-653A-4

  Query Match             99.1%;  Score 1679;  DB 10;  Length 325;
  Best Local Similarity   100.0%;  Pred. No. 1e-148;
  Matches  325;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHRLGSGGSGDGQFSWNLFSVPLPLPPLAGLLVQQIIF 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 CYISALVLSCLLTFLVLMRSLVTHRLGSGGSGDGQFSWNLFSVPLPLPPLAGLLVQQIIF 60

Qy         61 FLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVILQNMAAHWVFLETHDGHP 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 FLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVILQNMAAHWVFLETHDGHP 120

Qy        121 QLTNRRVLYAATFLLFPLNVLVGAMXXXCSPSIAIRHPTPGYYTYRNFLKIEVSQSHPAM 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 QLTNRRVLYAATFLLFPLNVLVGAMXXXCSPSIAIRHPTPGYYTYRNFLKIEVSQSHPAM 180

Qy        181 TAFCSLLLQAQSLLPRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGL 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TAFCSLLLQAQSLLPRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGL 240

Qy        241 AYTLLHNPTLQVFRKTALLGANGAQPCSSLPGSPPSITPAMQPAGPPDHXGXVEVCLHWE 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 AYTLLHNPTLQVFRKTALLGANGAQPCSSLPGSPPSITPAMQPAGPPDHXGXVEVCLHWE 300

Qy        301 PXXGSAPPTWLWESQQGFWRKKLVG 325
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Db        301 PXXGSAPPTWLWESQQGFWRKKLVG 325


RESULT 2
US-09-863-776-69
; Sequence 69, Application US/09863776
; Publication No. US20030198953A1
; GENERAL INFORMATION:
;  APPLICANT: Spytek, Kimberly A
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Mishra, Vishnu
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Spaderna, Steven K
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Li, Li
;  APPLICANT:  Taupier, Raymond J
;  APPLICANT:  Gangolli, Esha
;  TITLE OF INVENTION: No. US20030198953A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-020
;  CURRENT APPLICATION NUMBER: US/09/863,776
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: 09/540,763
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 60/206,679
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: 60/206,688
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: 60/206,829
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: 60/207,748
;  PRIOR FILING DATE: 2000-05-30
;  PRIOR APPLICATION NUMBER: 60/207,798
;  PRIOR FILING DATE: 2000-05-30
;  PRIOR APPLICATION NUMBER: 60/208,263
;  PRIOR FILING DATE: 2000-05-31
;  PRIOR APPLICATION NUMBER: 60/208,831
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: 60/209,451
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: 60/210,060
;  PRIOR FILING DATE: 2000-06-07
;  PRIOR APPLICATION NUMBER: 60/219,507
;  PRIOR FILING DATE: 2000-07-20
;  PRIOR APPLICATION NUMBER: 60/221,337
;  PRIOR FILING DATE: 2000-07-26
;  PRIOR APPLICATION NUMBER: 60/221,927
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: 60/263,135
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: 60/263,688
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/263,694
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 155
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 69
;   LENGTH: 560
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-863-776-69

  Query Match             65.5%;  Score 1110.5;  DB 10;  Length 560;
  Best Local Similarity   76.6%;  Pred. No. 3.4e-95;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |              | |  ||
Db        258 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 317

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                        |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        318 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 377

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              |||||||||||||||||||||||||||||||||||||||||||||
Db        378 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 437

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                  :::  |       ||||||||||||||||||||||||||||||||||||||||||
Db        438 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 497

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        498 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 557

Qy        264 AQP 266
              |||
Db        558 AQP 560


RESULT 3
US-10-104-047-2306
; Sequence 2306, Application US/10104047
; Publication No. US20030236392A1
; GENERAL INFORMATION:
;  APPLICANT: HELIX RESEARCH INSTITUTE
;  TITLE OF INVENTION: No. US20030236392A1el full length cDNA
;  FILE REFERENCE: H1-A0105
;  CURRENT APPLICATION NUMBER: US/10/104,047
;  CURRENT FILING DATE:  2002-03-25
;  PRIOR APPLICATION NUMBER:
;  PRIOR FILING DATE:
;  NUMBER OF SEQ ID NOS: 4096
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2306
;   LENGTH: 599
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-104-047-2306

  Query Match             65.5%;  Score 1110.5;  DB 15;  Length 599;
  Best Local Similarity   76.6%;  Pred. No. 3.7e-95;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;
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Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |            | |  ||
Db        297 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 356

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        357 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 416

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              |||||||||||||||||||||||||||||||||||||||||||||
Db        417 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 476

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                 :::  |      ||||||||||||||||||||||||||||||||||||||||||||
Db        477 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 536

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        537 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 596

Qy        264 AQP 266
              |||
Db        597 AQP 599
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RESULT 4
US-09-759-056-2
; Sequence 2, Application US/09759056
; Patent No. US20020156252A1
; GENERAL INFORMATION:
; APPLICANT: Pennica, Diane
; APPLICANT: Smith, Victoria
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: No. US20020156252A1el STRA6 Polypeptides
; FILE REFERENCE: GENENT.2827A2
; CURRENT APPLICATION NUMBER: US/09/759,056
; CURRENT FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/197089
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/175849
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/228914
; PRIOR FILING DATE: 2000-08-29
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-759-056-2

Query Match 65.5%; Score 1110.5; DB 9; Length 667;
Best Local Similarity 76.6%; Pred. No. 4.2e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

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Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |            | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              |||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                 :::  |      ||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
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Db        665 AQP 667
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RESULT 5
US-09-901-812-2
; Sequence 2, Application US/09901812
; Patent No. US20020173461A1
; GENERAL INFORMATION:
; APPLICANT: Pennica, Diane
; APPLICANT: Polakis, Paul
; APPLICANT: Szeto, Wayne
; TITLE OF INVENTION: UPREGULATION OF TUMOR ANTIGENS TO
; TITLE OF INVENTION: ENHANCE EFFICACY OF IMMUNOTHERAPY
; FILE REFERENCE: GENENT.083A
; CURRENT APPLICATION NUMBER: US/09/901,812
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/228,914
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: 09/759,056
; PRIOR FILING DATE: 2001-01-11
; PRIOR APPLICATION NUMBER: 60/175,849
; PRIOR FILING DATE: 2000-01-13
; PRIOR APPLICATION NUMBER: 60/197,089
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-901-812-2

Query Match 65.5%; Score 1110.5; DB 9; Length 667;
Best Local Similarity 76.6%; Pred. No. 4.2e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

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Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |            | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              |||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                 :::  |      ||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              ||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667
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RESULT 6
US-09-863-776-32
; Sequence 32, Application US/09863776
; Publication No. US20030198953A1
; GENERAL INFORMATION:
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Majumder, Kumud
; APPLICANT: Tchernev, Velizar T

```
;  APPLICANT:  Mishra, Vishnu
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Spaderna, Steven K
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Li, Li
;  APPLICANT:  Taupier, Raymond J
;  APPLICANT:  Gangolli, Esha
;  TITLE OF INVENTION: No. US20030198953A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-020
;  CURRENT APPLICATION NUMBER: US/09/863,776
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: 09/540,763
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 60/206,679
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: 60/206,688
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: 60/206,829
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: 60/207,748
;  PRIOR FILING DATE: 2000-05-30
;  PRIOR APPLICATION NUMBER: 60/207,798
;  PRIOR FILING DATE: 2000-05-30
;  PRIOR APPLICATION NUMBER: 60/208,263
;  PRIOR FILING DATE: 2000-05-31
;  PRIOR APPLICATION NUMBER: 60/208,831
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: 60/209,451
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: 60/210,060
;  PRIOR FILING DATE: 2000-06-07
;  PRIOR APPLICATION NUMBER: 60/219,507
;  PRIOR FILING DATE: 2000-07-20
;  PRIOR APPLICATION NUMBER: 60/221,337
;  PRIOR FILING DATE: 2000-07-26
;  PRIOR APPLICATION NUMBER: 60/221,927
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: 60/263,135
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: 60/263,688
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/263,694
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 155
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
;   LENGTH: 667
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-863-776-32

  Query Match             65.5%;  Score 1110.5;  DB 10;  Length 667;
  Best Local Similarity   76.6%;  Pred. No. 4.2e-95;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |              | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
              |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
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Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
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Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
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Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
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Db        665 AQP 667


RESULT 7
US-09-863-776-67
; Sequence 67, Application US/09863776
; Publication No. US20030198953A1
; GENERAL INFORMATION:
;  APPLICANT: Spytek, Kimberly A
;  APPLICANT:  Majumder, Kumud
;  APPLICANT:  Tchernev, Velizar T
;  APPLICANT:  Mishra, Vishnu
;  APPLICANT:  Padigaru, Muralidhara
;  APPLICANT:  Spaderna, Steven K
;  APPLICANT:  Shenoy, Suresh G
;  APPLICANT:  Rastelli, Luca
;  APPLICANT:  Li, Li
;  APPLICANT:  Taupier, Raymond J
;  APPLICANT:  Gangolli, Esha
;  TITLE OF INVENTION: No. US20030198953A1el Proteins and Nucleic Acids Encoding Same
;  FILE REFERENCE: 21402-020
;  CURRENT APPLICATION NUMBER: US/09/863,776
;  CURRENT FILING DATE:  2001-05-23
;  PRIOR APPLICATION NUMBER: 09/540,763
;  PRIOR FILING DATE: 2000-03-30
;  PRIOR APPLICATION NUMBER: 60/206,679
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: 60/206,688
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: 60/206,829
;  PRIOR FILING DATE: 2000-05-24
;  PRIOR APPLICATION NUMBER: 60/207,748
;  PRIOR FILING DATE: 2000-05-30
;  PRIOR APPLICATION NUMBER: 60/207,798
;  PRIOR FILING DATE: 2000-05-30
;  PRIOR APPLICATION NUMBER: 60/208,263
;  PRIOR FILING DATE: 2000-05-31
;  PRIOR APPLICATION NUMBER: 60/208,831
;  PRIOR FILING DATE: 2000-06-02
;  PRIOR APPLICATION NUMBER: 60/209,451
;  PRIOR FILING DATE: 2000-06-05
;  PRIOR APPLICATION NUMBER: 60/210,060
;  PRIOR FILING DATE: 2000-06-07
;  PRIOR APPLICATION NUMBER: 60/219,507
;  PRIOR FILING DATE: 2000-07-20
;  PRIOR APPLICATION NUMBER: 60/221,337
;  PRIOR FILING DATE: 2000-07-26
;  PRIOR APPLICATION NUMBER: 60/221,927
;  PRIOR FILING DATE: 2000-07-31
;  PRIOR APPLICATION NUMBER: 60/263,135
;  PRIOR FILING DATE: 2001-01-19
;  PRIOR APPLICATION NUMBER: 60/263,688
;  PRIOR FILING DATE: 2001-01-24
;  PRIOR APPLICATION NUMBER: 60/263,694
;  PRIOR FILING DATE: 2001-01-24
;  NUMBER OF SEQ ID NOS: 155
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
;   LENGTH: 667
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-863-776-67

  Query Match             65.5%;  Score 1110.5;  DB 10;  Length 667;
  Best Local Similarity   76.6%;  Pred. No. 4.2e-95;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
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Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
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Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
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Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
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Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
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Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
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Db        665 AQP 667
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RESULT 8
US-10-227-884-80
; Sequence 80, Application US/10227884
; Publication No. US20030027988A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C79
; CURRENT APPLICATION NUMBER: US/10/227,884
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
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; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 65.5%; Score 1110.5; DB 14; Length 667;
Best Local Similarity 76.6%; Pred. No. 4.2e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

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Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD-------------GQFSWNLFS 42
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Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                |||||||||||||||||||||||||||||||| |||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
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Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                 :::  |       |||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667
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RESULT 9
US-10-230-163-80
; Sequence 80, Application US/10230163
; Publication No. US20030036635A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C96
; CURRENT APPLICATION NUMBER: US/10/230,163
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
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; PRIOR APPLICATION NUMBER: 60/146963
; PRIOR FILING DATE: 1999-08-03
; PRIOR APPLICATION NUMBER: 60/149320
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/149638
; PRIOR FILING DATE: 1999-08-17
; PRIOR APPLICATION NUMBER: 60/151733
; PRIOR FILING DATE: 1999-08-31
; PRIOR APPLICATION NUMBER: 60/164418
; PRIOR FILING DATE: 1999-11-09
; PRIOR APPLICATION NUMBER: 60/166361
; PRIOR FILING DATE: 1999-11-16
; PRIOR APPLICATION NUMBER: 60/169445
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169495
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: 60/169835

Query Match 65.5%; Score 1110.5; DB 14; Length 667;
Best Local Similarity 76.6%; Pred. No. 4.2e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

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Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |            | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              |||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
               :::  |       ||||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667
```

RESULT 10
US-10-230-338-80
; Sequence 80, Application US/10230338
; Publication No. US20030044934A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C92
; CURRENT APPLICATION NUMBER: US/10/230,338
; CURRENT FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-230-338-80

Query Match 65.5%; Score 1110.5; DB 14; Length 667;
Best Local Similarity 76.6%; Pred. No. 4.2e-95;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

```
Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |            | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              |||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
               :::  |       ||||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667
```

RESULT 11
US-10-218-631-80
; Sequence 80, Application US/10218631
; Publication No. US20030045687A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME

```
;  FILE REFERENCE: P3530P1C14
;  CURRENT APPLICATION NUMBER: US/10/218,631
;  CURRENT FILING DATE:  2002-08-12
;  PRIOR APPLICATION NUMBER: 10/119,480
;  PRIOR FILING DATE: 2002-04-09
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/062287
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063549
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/064103
;  PRIOR FILING DATE: 1997-10-31
;  PRIOR APPLICATION NUMBER: 60/069873
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: 60/078910
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/079294
;  PRIOR FILING DATE: 1998-03-25
;  PRIOR APPLICATION NUMBER: 60/079656
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: 60/079728
;  PRIOR FILING DATE: 1998-03-27
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
;    LENGTH: 667
;    TYPE: PRT
;    ORGANISM: Homo Sapien
US-10-218-631-80

  Query Match             65.5%;  Score 1110.5;  DB 14;  Length 667;
  Best Local Similarity   76.6%;  Pred. No. 4.2e-95;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |              | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
              |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              |||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
               :::  |      ||||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667


RESULT 12
US-10-230-414-80
; Sequence 80, Application US/10230414
; Publication No. US20030050448A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Gerritsen, Mary
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stephan, Jean-Philippe F.
;  APPLICANT:  Watanabe, Colin L.
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3530P1C98
;  CURRENT APPLICATION NUMBER: US/10/230,414
;  CURRENT FILING DATE:  2002-08-28
;  PRIOR APPLICATION NUMBER: 10/119,480
;  PRIOR FILING DATE: 2002-04-09
;  PRIOR APPLICATION NUMBER: 60/059113
;  PRIOR FILING DATE: 1997-09-17
;  PRIOR APPLICATION NUMBER: 60/062287
;  PRIOR FILING DATE: 1997-10-17
;  PRIOR APPLICATION NUMBER: 60/063549
;  PRIOR FILING DATE: 1997-10-28
;  PRIOR APPLICATION NUMBER: 60/064103
;  PRIOR FILING DATE: 1997-10-31
;  PRIOR APPLICATION NUMBER: 60/069873
;  PRIOR FILING DATE: 1997-12-17
;  PRIOR APPLICATION NUMBER: 60/078910
;  PRIOR FILING DATE: 1998-03-20
;  PRIOR APPLICATION NUMBER: 60/079294
;  PRIOR FILING DATE: 1998-03-25
;  PRIOR APPLICATION NUMBER: 60/079656
;  PRIOR FILING DATE: 1998-03-26
;  PRIOR APPLICATION NUMBER: 60/079728
;  PRIOR FILING DATE: 1998-03-27
;  Remaining Prior Application data removed - See File Wrapper or PALM.
;  NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
;    LENGTH: 667
;    TYPE: PRT
;    ORGANISM: Homo Sapien
US-10-230-414-80

  Query Match             65.5%;  Score 1110.5;  DB 14;  Length 667;
  Best Local Similarity   76.6%;  Pred. No. 4.2e-95;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |              | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
              |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              |||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
               :::  |      ||||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667


RESULT 13
US-10-232-224-80
; Sequence 80, Application US/10232224
; Publication No. US20030065147A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Gerritsen, Mary
```

```
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C111
; CURRENT APPLICATION NUMBER: US/10/232,224
; CURRENT FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
;   LENGTH: 667
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-232-224-80

  Query Match            65.5%;  Score 1110.5;  DB 14;  Length 667;
  Best Local Similarity  76.6%;  Pred. No. 4.2e-95;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |              | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
              |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------ 149
              |||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                 :::  |      |||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667


RESULT 14
US-10-216-159A-80
; Sequence 80, Application US/10216159A
; Publication No. US20030069397A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C6
; CURRENT APPLICATION NUMBER: US/10/216,159A
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
;   LENGTH: 667
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-216-159A-80

  Query Match            65.5%;  Score 1110.5;  DB 14;  Length 667;
  Best Local Similarity  76.6%;  Pred. No. 4.2e-95;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |              | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
              |||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------ 149
              |||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                 :::  |      |||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667
```

```
RESULT 15
US-10-218-849-80
; Sequence 80, Application US/10218849
; Publication No. US20030073814A1
; GENERAL INFORMATION:
;  APPLICANT: Baker, Kevin P.
;  APPLICANT:  Desnoyers, Luc
;  APPLICANT:  Gerritsen, Mary
;  APPLICANT:  Goddard, Audrey
;  APPLICANT:  Godowski, Paul J.
;  APPLICANT:  Grimaldi, J. Christopher
;  APPLICANT:  Gurney, Austin L.
;  APPLICANT:  Smith, Victoria
;  APPLICANT:  Stephan, Jean-Philippe F.
;  APPLICANT:  Watanabe, Colin L.
;  APPLICANT:  Wood, William I.
;  TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
;  TITLE OF INVENTION:  ACIDS ENCODING THE SAME
;  FILE REFERENCE: P3530P1C11
;  CURRENT APPLICATION NUMBER: US/10/218,849
;  CURRENT FILING DATE:  2002-08-12
;  Prior Application removed - See File Wrapper or Palm
;  NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 80
;   LENGTH: 667
;   TYPE: PRT
;   ORGANISM: Homo Sapien
US-10-218-849-80

  Query Match             65.5%;  Score 1110.5;  DB 14;  Length 667;
  Best Local Similarity   76.6%;  Pred. No. 4.2e-95;
  Matches  232;  Conservative    4;  Mismatches   30;  Indels   37;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              |||||||||||||||||||||||||     |  | : |              | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                |||||||||||||||||||||||||||||| ||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
              ||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                  :::  |      ||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
              |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
              |||
Db        665 AQP 667


Search completed: February  8, 2005, 13:45:13
Job time : 109.54 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 13:29:35 ; Search time 31.6317 Seconds
(without alignments)
988.580 Million cell updates/sec

Title: US-09-816-653A-4
Perfect score: 1695
Sequence: 1 CYISALVLSCLLTFLVLMRS.....APPTWLWESQQGFWRKKLVG 325

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	96.5	5.7	593	2	A71361	probable thiamin A
2	93	5.5	2016	2	A38195	sodium channel pro
3	91.5	5.4	581	2	T44942	cytochrome-c oxida
4	90.5	5.3	625	2	S18420	regulatory protein
5	89.5	5.3	107	2	C91079	probable cytochrom
6	89.5	5.3	107	2	D85924	probable cytochrom
7	89.5	5.3	268	2	S34364	hypothetical prote
8	89	5.3	3164	1	WMBEH6	UL36 protein - hum
9	88.5	5.2	107	2	A65056	hypothetical prote
10	88.5	5.2	395	2	AB1061	probable innner me
11	87	5.1	621	2	I49199	growth factor rece
12	86.5	5.1	301	2	G83556	hypothetical prote
13	86	5.1	528	2	AI0359	iron(III)-transpor
14	86	5.1	582	2	A87673	conserved hypothet
15	86	5.1	614	2	S40085	hypothetical prote
16	85.5	5.0	340	2	T18704	hypothetical prote
17	85.5	5.0	402	2	AB0854	probable membrane
18	84.5	5.0	166	2	T01263	hypothetical prote
19	84.5	5.0	230	2	T11290	cytochrome-c oxida
20	84.5	5.0	332	2	B81252	NADH2 dehydrogenas
21	84.5	5.0	377	2	F95948	probable acyltrans
22	84.5	5.0	636	2	T35182	probable ABC-type
23	84.5	5.0	1011	2	T07712	probable ABC-type
24	84	5.0	291	2	AG1846	sulfate transport
25	84	5.0	321	2	T11088	NADH2 dehydrogenas
26	84	5.0	477	2	D83617	probable amino aci
27	84	5.0	527	1	QRSEUB	sfuB protein - Ser
28	84	5.0	585	2	B75265	probable acid-CoA
29	83	4.9	222	1	S75137	hypothetical prote
30	83	4.9	297	2	AB2436	permease protein o
31	83	4.9	394	2	T31891	hypothetical prote
32	83	4.9	487	2	F72126	ct339 hypothetical
33	83	4.9	596	2	F75302	ATP-dependent DNA
34	83	4.9	1089	2	E82987	hypothetical prote
35	83	4.9	1840	1	CHRTM1	sodium channel pro
36	82.5	4.9	228	2	C38941	cytochrome-c oxida
37	82.5	4.9	393	2	B86644	transporter ybfD [
38	82.5	4.9	888	2	JC5399	dual leucine zippe
39	82.5	4.9	3005	2	T08841	polyprotein - dour
40	82	4.8	335	2	A87135	probable membrane
41	82	4.8	516	2	AB3088	MFS permease [prol
42	82	4.8	516	2	G98198	proline/betaine tr
43	82	4.8	627	2	A98344	hypothetical prote
44	82	4.8	627	2	AF2938	conserved hypothet
45	81.5	4.8	315	2	AG3535	dipeptide transpor

ALIGNMENTS

RESULT 1
A71361
probable thiamin ABC transporter, permease protein - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
C;Accession: A71361
R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwi
rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McD
they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
A;Reference number: A71250; MUID:98332770; PMID:9665876
A;Accession: A71361
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-593 <COL>
A;Cross-references: UNIPROT:O83179; GB:AE001199; GB:AE000520; NID:g3322402; PIDN:AAC651
A;Experimental source: strain Nichols
C;Genetics:
A;Gene: TP0143

Query Match 5.7%; Score 96.5; DB 2; Length 593;
Best Local Similarity 23.0%; Pred. No. 1.7;
Matches 61; Conservative 29; Mismatches 86; Indels 89; Gaps 12;

```
Qy          3 ISALVLSCLL----TFLVLMRSLVTHRLGSGGSGDGQFSWNLFSVPLPLPPLAGLLVQQI 58
              : : ||:| :     |  : |||    |             | ::|| :|||
Db        120 LCSAVLACAVGFGAAFFFVKRSLRARALFPA----------LCAIPLAIPPL-------- 161

Qy         59 IFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPF-----------------WLTLALA 100
                | |||||:      |:| |  |:| : |                    |    ||
Db        162 -----TMALAFLLSF----GKNGLCTRTLGTLWGVSTPRTFLYSASGVVIAHAWYNFPLA 212

Qy        101 VILQNMAAHWVFLETHDGHPQLTNR--RVLYAATFLLFPLNVLVGAMXXX-------CSP 151
              : :   | : :  :  |    |  |  || |  |     |  | ||:          |
Db        213 LAIIARAWNTISADAEDAARLLGARAYRVFYTIT-----LPALAGALRSSFLVIFLYCFF 267

Qy        152 SIAI-------RHPTPGYYTYRNFLKIEVSQSHP-------AMTAFCSLLL--------- 188
              |: :          |     ||:   |    :||       : | :  |::
Db        268 SLMMVLLLGGTTFTTLEVELYRS---IRTQAAHPYASTLALSQTFYALLMIWGVSTEESQ 324

Qy        189 QAQSLLPRTMAAPQDSLRPGEEDEG 213
              |||| : ||   |  |::   |  |
Db        325 QAQSCVARTRPLPTQSIQGNIERIG 349
```

RESULT 2
A38195
sodium channel protein hHI, cardiac - human
N;Alternate names: tetrodotoxin-insensitive, voltage-dependent sodium channel, TTX-I Na
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

```
C;Accession: A38195
R;Gellens, M.E.; George Jr., A.L.; Chen, L.Q.; Chahine, M.; Horn, R.; Barchi, R.L.; Kall
Proc. Natl. Acad. Sci. U.S.A. 89, 554-558, 1992
A;Title: Primary structure and functional expression of the human cardiac tetrodotoxin-i
A;Reference number: A38195; MUID:92115699; PMID:1309946
A;Accession: A38195
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-2016 <GEL>
A;Cross-references: UNIPROT:Q14524; GB:M77235; NID:g184038; PIDN:AAA58644.1; PID:g184039
A;Experimental source: heart
C;Superfamily: sodium channel protein
C;Keywords: cardiac muscle; duplication; glycoprotein; heart; ion transport; sodium chan

  Query Match             5.5%;  Score 93;  DB 2;  Length 2016;
  Best Local Similarity   23.8%;  Pred. No. 14;
  Matches   67;  Conservative   31;  Mismatches  113;  Indels   70;  Gaps   13;

Qy         35 QPSWNLFSVPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFW 94
              |  ||:|           ::|    :  || : :: |    ||     ||     |  |||
Db        778 QQGWNIFD---------SIIVILSLMELGLSRMSNL---SVLRSFRLLRVFKLAKSWPTL 825

Qy         95 ----------------LTLALAVILQNMAAHWV------FLETHDGHPQLTNR---RVLY 129
                            ||| ||:|:   |   :      : |  |     |  |      :
Db        826 NTLIKIIGNSVGALGNLTLVLAIIVFIFAVVGMQLFGKNYSELRDSDSGLLPRWHMMDFF 885

Qy        130 AATFLLFPLNVLVGAMXXXCSPSIAIRHPTPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQ 189
              |  ::|   :| |          : :   :          || : |  :   :  | :|||
Db        886 HAFLIIF--RILCGEWIETMWDCMEVSGQS---LCLLVFLLVMVIGNLVVLNLFLALLLS 940

Qy        190 AQSLLPRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLL-HNP 248
              : |          |:|   :||  |  ||   ::|:  |       |  |     || | |
Db        941 SFS---------ADNLTAPDEDREMNNLQL--ALARIQRGLRFVKRTTWDFCCGLLRHRP 989

Qy        249 TLQVFRKTALLGANGAQP-CSSLPGSPPSITPAMQPAGPPD 288
                  :| | | | |  | | : | |||          ||:
Db        990 -----QKPAALAAQGQLPSCIATPYSPP----------PPE 1015


RESULT 3
T44942
cytochrome-c oxidase (EC 1.9.3.1) chain I [similarity] - Natronobacterium pharaonis
N;Alternate names: ba3-type cytochrome-c oxidase chain I
C;Species: Natronobacterium pharaonis
C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C;Accession: T44942
R;Mattar, S.; Engelhard, M.
Eur. J. Biochem. 250, 332-341, 1997
A;Title: Cytochrome ba3 from Natronobacterium pharaonis: An archaeal four-subunit cytoch
A;Reference number: Z22876; MUID:98088958; PMID:9428682
A;Accession: T44942
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-581 <MAT>
A;Cross-references: UNIPROT:O07289; EMBL:Y10500; PIDN:CAA71525.1
A;Experimental source: strain SP1/28
C;Genetics:
A;Gene: cbaA
C;Superfamily: cytochrome-c oxidase chain I; cytochrome-c oxidase chain I homology
C;Keywords: copper; electron transfer; heme; iron; magnesium; membrane-associated comple
F;228-232/Cross-link: 1'-histidyl-3'-tyrosine (His-Tyr) #status predicted
F;379/Binding site: heme a3 iron (His) (axial ligand) #status predicted

  Query Match             5.4%;  Score 91.5;  DB 2;  Length 581;
  Best Local Similarity   26.6%;  Pred. No. 4.5;
  Matches   63;  Conservative   32;  Mismatches   89;  Indels   53;  Gaps   15;

Qy          6 LVLSCLLTFLVLMRSLVTHRLGSGGSGDGQFSWNLFSVPLPLPPLAGLLVQQIIFFLGTT 65
              |:|  |||   :: |:       |||  | | | | ::|   |   |: :  ::|
Db        300 LLLPSLLTAFTVVASMEHGARQRGGS--GYFGW-LRALPWRDPVFTGMALAGLMF----A 352

Qy         66 ALAFLVLMPVLHGRNLLFFRSLESSW----PFWLTLALAVILQNMAAHWVFLETHDGHPQ 121
                 | ||  :  |  | |: :   : ::|     | ||:  || |  ||  : ||      ||
Db        353 AAAFSGM--VNAGMNINYL--VHNTWWVVGHFHLTVGTAVALTFMAVSYWFL------PQ 402

Qy        122 LTNRR-----VLYAATFLLF-PLNVLVGAMXXXCSPSIAIRHPTPGYYTYRNFLKIEVSQ 175
                 :| ::      |  |    | |  :  :  ||        :  |   |    ||||  : |::
Db        403 ITGKKLWGKSVALAQVVLWFVGMTFMSNAMHRSGLAGMPRRTAEP---QYRNF-EFEMAA 458

Qy        176 SH----PAMTAFCSLLLQAQSLL---------------PRTMAAPQ--DSLRPGEED 211
                     |       :||   :||                 | |: | :  |:|  | ||
Db        459 GSLGELNAQVVLGGILLFVSTLLFVLVVVMTVLGDKAEPGTLPANEYADTL-SGPED 514


RESULT 4
S18420
regulatory protein nifA - Azospirillum brasilense
C;Species: Azospirillum brasilense
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S18420
R;Liang, Y.Y.; Kaminski, P.A.; Elmerich, C.
Mol. Microbiol. 5, 2735-2744, 1991
A;Title: Identification of a nifA-like regulatory gene of Azospirillum brasilense Sp7 ex
A;Reference number: S18420; MUID:92140038; PMID:1779763
A;Accession: S18420
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-625 <LIA>
A;Cross-references: UNIPROT:P30667; EMBL:X60714; NID:g38677; PIDN:CAA43126.1; PID:g38678
C;Genetics:
A;Gene: nifA
C;Superfamily: Response regulator (sigma54-dependent transcriptional activator), FhlA ty
C;Keywords: DNA binding; P-loop; transcription regulation
F;205-426/Domain: RNA polymerase sigma factor interaction domain homology <SFI>
F;233-240/Region: nucleotide-binding motif A (P-loop) #status atypical
F;300-304/Region: nucleotide-binding motif B

  Query Match             5.3%;  Score 90.5;  DB 2;  Length 625;
  Best Local Similarity   27.7%;  Pred. No. 5.9;
  Matches   48;  Conservative    9;  Mismatches   55;  Indels   61;  Gaps    9;

Qy        184 CSLLLQAQSLL--PRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGA-------RPG---- 230
              |||  |   |:|   ||: |    | |              ||  ||       |||
Db        447 CSLNLCNSSVLFQYRTLGASVGGLAP-------------SMGPGAINRVPPGRPGGPAA 492

Qy        231 --------------------AXRGRARWGLAYTLLHNPTLQVFRKTALLGANG----AQP 266
                                 | |||     |  ::  |   : |: |  | :|    | |
Db        493 ANAPKTPAMPAPVPEPAGAAAARGRP----ARRVVPRPLAGLRRRPA--GGSGPPDPACP 546

Qy        267 CSSLPGSPPSITPAMQPAGPPDHXGXVEVCLHWEPXXGSAPPTWLWESQQGFW 319
              | |    ||   |    | ||      || |  ||  ||      ||  ::  |
Db        547 CPSRAPLPPQAPPPSPAAAPPP---AAEVPLD-EPESGSLRDRLLWAMERTGW 595


RESULT 5
C91079
probable cytochrome oxidase subunit [imported] - Escherichia coli (strain O157:H7, subst
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C;Accession: C91079
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: C91079
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <HAY>
A;Cross-references: UNIPROT:Q8X7Y2; GB:BA000007; PIDN:BAB37026.1; PID:g13363074; GSPDB:G
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs3603
C;Superfamily: uncharacterized conserved protein YPO3363

  Query Match             5.3%;  Score 89.5;  DB 2;  Length 107;
```

```
  Best Local Similarity   24.6%;  Pred. No. 0.96;
  Matches   28;  Conservative   21;  Mismatches   34;  Indels   31;  Gaps    5;

Qy         33 DGQFSWNLFSVPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVL-HGRNLLFFRSLESSW 91
              | : :|:           | | :|       |  :  | : ||:| :| | |||     :|
Db         18 DEETTWS----------LPGAVV-------GFISWLFALAMPMLIYGSNTLFF--FIYTW 58

Qy         92 PFWLTLALAVILQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAM 145
              ||:| |    ::  :| |            | : :: |:  | |  : :: ||:
Db         59 PFFLALMPVAVVVGIALH----------SLMDGKLRYSIVFTLMTVGIMFGAL 101


RESULT 6
D85924
probable cytochrome oxidase subunit ygbE [imported] - Escherichia coli (strain O157:H7,
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: D85924
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: D85924
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-107 <STO>
A;Cross-references: UNIPROT:Q8X7Y2; GB:AE005174; NID:g12517203; PIDN:AAG57856.1; GSPDB:G
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: ygbE
C;Superfamily: uncharacterized conserved protein YPO3363

  Query Match             5.3%;  Score 89.5;  DB 2;  Length 107;
  Best Local Similarity   24.6%;  Pred. No. 0.96;
  Matches   28;  Conservative   21;  Mismatches   34;  Indels   31;  Gaps    5;

Qy         33 DGQFSWNLFSVPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVL-HGRNLLFFRSLESSW 91
              | : :|:           | | :|       |  :  | : ||:| :| | |||     :|
Db         18 DEETTWS----------LPGAVV-------GFISWLFALAMPMLIYGSNTLFF--FIYTW 58

Qy         92 PFWLTLALAVILQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAM 145
              ||:| |    ::  :| |            | : :: |:  | |  : :: ||:
Db         59 PFFLALMPVAVVVGIALH----------SLMDGKLRYSIVFTLMTVGIMFGAL 101


RESULT 7
S34364
hypothetical protein X - Salmonella typhimurium (fragment)
C;Species: Salmonella typhimurium
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct-1999
C;Accession: S34364
R;Persson, B.C.; Bjork, G.R.
submitted to the EMBL Data Library, June 1993
A;Description: Isolation of a gene (miaE) involved in hydroxylation of ms2io6A in tRNA o
A;Reference number: S34359
A;Accession: S34364
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-268 <PER>
A;Cross-references: EMBL:X73368; NID:g312705; PIDN:CAA51785.1; PID:g312711

  Query Match             5.3%;  Score 89.5;  DB 2;  Length 268;
  Best Local Similarity   26.2%;  Pred. No. 2.7;
  Matches   37;  Conservative   20;  Mismatches   45;  Indels   39;  Gaps    6;

Qy          5 ALVLSCLLTFLVLMRSLVTHRLGSGGSGDGQFSWNLFSVPLPLPPLAGLLVQQIIFFLGT 64
              || :| || |:: : ||      |  | |     : ||         |||:  || |:
Db         27 ALFISVLLVFIIYIVSLSLIEHGHPGLG-----FTLF----------GLLI-AIIPFMAV 70

Qy         65 TALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVILQNMAAHWVFLETHDGHPQLTN 124
                | :  :|  |:| :  |  |:  :|  |    || |:|  | |
Db         71 KGLQYQAMMTSLNGVHFGFQCSMRRAW--WYMFALPVLL--MVA---------------- 110

Qy        125 RRVLYAATFLLFPLNVLVGAM 145
                 ||   :::  : : || :
Db        111 ---LYIVLYIISLVTIAVGGL 128


RESULT 8
WMBEH6
UL36 protein - human herpesvirus 1 (strain 17)
C;Species: human herpesvirus 1
C;Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 09-Jul-2004
C;Accession: I30085
R;McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; Perr
J. Gen. Virol. 69, 1531-1574, 1988
A;Title: The complete DNA sequence of the long unique region in the genome of herpes sim
A;Reference number: A30083; MUID:88274327; PMID:2839594
A;Accession: I30085
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-3164 <MCG>
A;Cross-references: UNIPROT:P10220; GB:X14112; NID:g1944536; PIDN:CAA32311.1; PID:g5953
C;Genetics:
A;Gene: UL36
C;Superfamily: varicella-zoster virus gene 22 protein

  Query Match             5.3%;  Score 89;  DB 1;  Length 3164;
  Best Local Similarity   36.9%;  Pred. No. 51;
  Matches   24;  Conservative    4;  Mismatches   17;  Indels   20;  Gaps    3;

Qy        247 NPTLQVFRKTALLGANGAQPCSSLPGSPPSITPAMQPAGPPDHXGXVEVCLHWEPXXGSA 306
              :||  |       || | |:| || |  |    ||:||  ||              |  |
Db       2824 DPTAPV------LGRNPAEPTSSSPAGPSPPPPAVQPVAPP-------------PTSG-P 2863

Qy        307 PPTWL 311
              |||:|
Db       2864 PPTYL 2868


RESULT 9
A65056
hypothetical protein in surE-cysC intergenic region - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C;Accession: A65056
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A65056
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-107 <BLAT>
A;Cross-references: UNIPROT:P46141; GB:AE000358; GB:U00096; NID:g2367156; PIDN:AAC75791
A;Experimental source: strain K-12, substrain MG1655
C;Genetics:
A;Gene: ygbE
C;Superfamily: uncharacterized conserved protein YPO3363

  Query Match             5.2%;  Score 88.5;  DB 2;  Length 107;
  Best Local Similarity   24.6%;  Pred. No. 1.2;
  Matches   28;  Conservative   21;  Mismatches   34;  Indels   31;  Gaps    5;

Qy         33 DGQFSWNLFSVPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVL-HGRNLLFFRSLESSW 91
              | : :|:           | | :|       |  :  | : ||:| :| | |||     :|
Db         18 DEETTWS----------LPGAVV-------GFISWLFALAMPMLIYGSNTLFF--FIYTW 58

Qy         92 PFWLTLALAVILQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAM 145
              ||:| |    ::  :| |            | : :: |:  | |  : :: ||:
Db         59 PFFLALMPVAVVVGIALH----------SLMDGKLRYSIVFTLVTVGIMFGAL 101


RESULT 10
```

AB1061
probable innner membrane protein STY4813 [imported] - Salmonella enterica subsp. enteric
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB1061
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB1061
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-395 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD06935.1; PID:g16505583; GSPDB:GN00176
C;Genetics:
A;Gene: STY4813

Query Match 5.2%; Score 88.5; DB 2; Length 395;
Best Local Similarity 26.2%; Pred. No. 5.2;
Matches 37; Conservative 20; Mismatches 45; Indels 39; Gaps 6;

```
Qy          5 ALVLSCLLTFLVLMRSLVTHRLGSGGSGDGQFSWNLFSVPLPLPPLAGLLVQQIIFFLGT 64
              || :| || |:: : ||      |  | |     : ||          |||:  || |:
Db         73 ALFISVLLVFIIYIVSLSFIEHGHPGLG-----FTLF----------GLLI-AIIPFMAV 116

Qy         65 TALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVILQNMAAHWVFLETHDGHPQLTN 124
                | :  :|  |:| :  |  |:  :|  |   || |:|  | |
Db        117 KGLQYQAMMTSLNGVHFGFQCSMRRAW--WYMFALPVLL--MVA--------------- 156

Qy        125 RRVLYAATFLLFPLNVLVGAM 145
                ||   :::  : : || :
Db        157 ---LYIVLYIISLVTIAVGGL 174
```

RESULT 11
I49199
growth factor receptor binding protein Grb10 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I49199
R;Ooi, J.; Yajnik, V.; Immanuel, D.; Gordon, M.; Moskow, J.J.; Buchberg, A.M.; Margolis,
Oncogene 10, 1621-1630, 1995
A;Title: The cloning of Grb10 reveals a new family of SH2 domain proteins.
A;Reference number: I49199; MUID:95249278; PMID:7731717
A;Accession: I49199
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-621 <RES>
A;Cross-references: UNIPROT:Q60760; EMBL:U18996; NID:g841209; PIDN:AAB53687.1; PID:g8412
C;Genetics:
A;Gene: Grb10
C;Keywords: growth factor receptor
F;520-614/Domain: SH2 homology <SH2B>

Query Match 5.1%; Score 87; DB 2; Length 621;
Best Local Similarity 21.7%; Pred. No. 12;
Matches 38; Conservative 28; Mismatches 59; Indels 50; Gaps 8;

```
Qy        172 EVSQSHPAMTAFCSL--------LLQ----------AQSLLPRTMAAPQDSLRPGEEDEG 213
              ::: |  :: : |::         ||:          | |   :  |:|:  ::  :
Db          4 DINSSVESLNSACNMQSDTDTAPLLEDGQHASNQGAASSSRGQPQASPRQKMQRSQPVHI 63

Qy        214 MQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANGAQPCSSLPGS 273
              :: || :|   : |             :   : ||  :       | ||          |||
Db         64 LRRLQEEDQQLRTA-------------SLPAIPNPFPE------LTGA--------APGS 96

Qy        274 PPSITPAM---QPAGPP-DHXGXVEVCLHWEPXXGSAP-PTWLWESQQGFWRKKL 323
              |||: |:     |: ||  | |  |  :  |   |:      | |:   ||    ||
Db         97 PPSVAPSSLPPPPSQPPAKHCGRCEKWIPGENTRGNGKRKIWRWQFPPGFQLSKL 151
```

RESULT 12
G83556
hypothetical protein PA0702 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: G83556
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: G83556
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-301 <STO>
A;Cross-references: UNIPROT:Q9I5M4; GB:AE004506; GB:AE004091; NID:g9946584; PIDN:AAG0409
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: PA0702

Query Match 5.1%; Score 86.5; DB 2; Length 301;
Best Local Similarity 21.9%; Pred. No. 5.7;
Matches 61; Conservative 27; Mismatches 105; Indels 85; Gaps 10;

```
Qy         58 IIFFLGTTALAFLV----------------LMPVLHGR-----NLL------------ 82
              :  |||   |:||                 |  |||       | |
Db         36 VALFLGALGLSFLAERRLPYQPRWNRPHADRLRDVLHASVNESLNALGILALPLLAGVLG 95

Qy         83 FFRSLESSWPFWLTLALAVILQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLV 142
              |:     :|| || | ||::| ::    |   :|                : ||: |:
Db         96 FWPVWPQAWPLWLQLLLAIVLADLGITLVHYASH----------RSALLWRLH--- 138

Qy        143 GAMXXXCSPSIAIRHPTPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQ 202
                      |: |     | :   :|  :     |:      |||     :|:|:||
Db        139 ----------AVHHSVQRLYGFNGLMKHPLHLGLEALGGTLPLLLLG---VPQTVAALL 184

Qy        203 DSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLH---------NPTLQVF 253
                     |:|||    ::    | |  |    |   : | |           | |
Db        185 AFA------IGIQLLLQHSNV--DMRIGGLRHVFAWAPLHRLHHIRYGRAGDVNFALFFS 236

Qy        254 RKTALLGANGAQPCSSLPGSPPSITPAMQPAGPPDHXG 291
                   |||    :|   |  :   |    ||  | |: |
Db        237 VWDRLLGTALHRPDYRLDSTDMGI--GDQPDYPRDYAG 272
```

RESULT 13
AI0359
iron(III)-transport system permease sfuB [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AI0359
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AI0359
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-528 <KUR>
A;Cross-references: UNIPROT:Q8ZCM3; GB:AL590842; PIDN:CAC92204.1; PID:g15980916; GSPDB:C
C;Genetics:
A;Gene: sfuB
C;Superfamily: sfuB protein

Query Match 5.1%; Score 86; DB 2; Length 528;
Best Local Similarity 22.3%; Pred. No. 12;
Matches 78; Conservative 31; Mismatches 129; Indels 112; Gaps 15;

```
Qy          6 LVLSCLLTFLVLMRSLVTHRLGSGGSGDGQFSWNLFSVPLPLPPLAGLLVQQIIFFLGTT 65
              | | ||   ||   |   ||    |||  :                    :| :: :||:
Db        244 LALCCLGLLLVEATSRGYHRYARVGSGTPR--------------------RQTVYSMGTS 283

Qy         66 ALAFLVLMPVLHGRNLLFFRSLESSWPF-----WLT---------------------LAL 99
                :|:|:|         :|    ||     ||:                       |||
Db        284 LTLLCLLLPLL-------ITTLSLGVPFITLMRWLSIGGIDIWLNPELLPALKQTLGLAL 336

Qy        100 --AVILQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXCSPSIAIRH 157
                |||:   |    :|    :|   :|    |     :  : | | :      :| ||
Db        337 SGAVIITLCAIPMAWLSVR--YPGRLHR----AMEGCYYVTSSLPGIVVALALVTITIRI 390

Qy        158 PTPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQDSLRPGEEDEGMQLL 217
              | |                 | |  ||       || :     ||| |     ::|
Db        391 ARPLY----------------QTEFTVLLAYLLMFTPRALI----SLRAGIAQAPVELE 429

Qy        218 QTKDSMAKG-----------ARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANGAQ 265
              ,   |: :             | |||  | |   | :  : |        | ||  || :
Db        430 NVARSLGRTPTQAMLSTTLRLAAPGAAAGAA---LVFLAISNE----LTATLLLAPNGTR 482

Qy        266 PCSSLPGSPPSITPAMQPAGPPDHXGXVEVCLHWEPXXGSAPPTWLWESQ 315
              ::  |    :     |  |     : | |       | | |||  ||
Db        483 TLAT--GFWALTSEIDYVAAAP--YAFLMVAL-------SLPLTWLLYSQ 521
```

RESULT 14
A87673
conserved hypothetical protein CC3419 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: A87673
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: A87673
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-582 <STO>
A;Cross-references: UNIPROT:Q9A2Y7; GB:AE005673; NID:g13425133; PIDN:AAK25381.1; GSPDB:G
C;Genetics:
A;Gene: CC3419

Query Match 5.1%; Score 86; DB 2; Length 582;
Best Local Similarity 24.3%; Pred. No. 13;
Matches 74; Conservative 30; Mismatches 113; Indels 88; Gaps 14;

```
Qy         62 LGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVILQNMAAHWVFL---ETHDG 118
              :| | | :|: : || |    |          | | | |   :| : ||  : |      ||
Db        220 VGLTLLGWLLPLMVLIGGGFLATLPFTGLAPLWGTKAATALLLSAAAALILLINAAYQDG 279

Qy        119 H--PQLTNRRVLYAATFLLFPLNVLVG-------------------------AMXXXCSP 151
                 | |         |  || |: :| |                        |:
Db        280 EEPPHLIPCLAARIAGLLLIPIVILAGYALWLRIDQYGLTPERVVAGVYLVVAIGFTAGY 339

Qy        152 SIAIRHPTPGYYTYRNFLKIEVSQSHPAMTAFCSLLL----------------QAQSLL 194
              ::|   | |       ::|  : :::| | | | |||                | : |
Db        340 ALAAVKPGP-------WMK-PLERTNPIMAAACVLLLIALFTPIANPARLSVASQVKRLE 391

Qy        195 PRTMAAPQ--------DSLRPGEEDEGMQLLQTKDS--MAKGARPGAXRGRARWGLAYTL 244
                :|| :         |: | |   | :  |:|  :  :|| ||  |          | |
Db        392 SGEVAADKFDFQFLRFDAGRYGR--EALDRLKTHPNAEIAKRARDAA---------ASTE 440

Qy        245 LHNPTLQV---FRKTALLGANGAQPCS------SLPGSPPSITPAMQ-PA--GPPDHXGX 292
                |  ::   |:  |:  |  | | |       | |         ||| ||     |  |
Db        441 KQYPAGEIRPDFKAMAVYPAGKALPQSFVAQDWSQPSGSNCTAIAMQCPALVADVDADGK 500

Qy        293 VEVCL 297
                || |
Db        501 DEVLL 505
```

RESULT 15
S40085
hypothetical protein 4 - Lactococcus lactis
C;Species: Lactococcus lactis
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C;Accession: S40085
R;Eaton, T.J.; Shearman, C.; Gasson, M.
submitted to the EMBL Data Library, December 1993
A;Description: Cloning and sequence analysis of the DNAK gene region of Lactococcus lac
A;Reference number: S40082
A;Accession: S40085
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-614 <EAT>
A;Cross-references: UNIPROT:P42377; EMBL:X76642; NID:g435489; PIDN:CAA54090.1; PID:g435

Query Match 5.1%; Score 86; DB 2; Length 614;
Best Local Similarity 19.9%; Pred. No. 14;
Matches 49; Conservative 35; Mismatches 74; Indels 88; Gaps 11;

```
Qy          5 ALVLSCLLTFLVLMRSLVTHRLGSGGSGDGQFSWNLFSV------PLPLPPLAGLLVQQI 58
              :|: ||    ||||:  :             | | |||:      |     | ||
Db        332 SLIFSCFSLVLVLMQLPI------------FPWKLFSIFTIVQDPARFSTLFGLF---- 374

Qy         59 IFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVILQNMAAHWVFLETHDG 118
                :||: ::::|:|         :     ::||: | ||   :                |
Db        375 ------SALSLVLILPIL-------LDKISGKTSYYLTIGLLVIFSIL----------G 410

Qy        119 HPQLTNR-----RVLYAA----------TFLLFPLNVLVGAMXXXCSPSIAIRHPTPGYY 163
                :  ||     : |:|:          ::  | :: :|       |  :   |  |
Db        411 FAEFRNRIQKGSQPLFASAQSLLNKTPFNYMENPDSIAIGEYL----PQVIGSHNQPYEK 466

Qy        164 TYRNFLKIE--VSQSHPAMTAFCSLLLQAQSLLPRTMAAPQDSLRPGEEDEGMQLLQTKD 221
              | : | | :      : |||      |  :  ||  :|                : :|  |
Db        467 TIQQFYKDKNVYGMRNQAMT-----YLSQRGKLPEGLA--------------KSIQISD 506

Qy        222 SMAKGA 227
                ||:
Db        507 YSKKGS 512
```

Search completed: February 8, 2005, 13:41:06
Job time : 34.1317 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: February 8, 2005, 13:21:20 ; Search time 142.653 Seconds
(without alignments)
1166.650 Million cell updates/sec

Title: US-09-816-653A-4
Perfect score: 1695
Sequence: 1 CYISALVLSCLLTFLVLMRS.....APPTWLWESQQGFWRKKLVG 325

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1110.5	65.5	560	2	Q7L9G1	Q7l9g1 homo sapien
2	1110.5	65.5	667	2	Q8TB21	Q8tb21 homo sapien
3	1110.5	65.5	667	2	Q9BX79	Q9bx79 homo sapien
4	1110.5	65.5	708	2	Q7Z3U9	Q7z3u9 homo sapien
5	1106.5	65.3	658	2	Q9BX78	Q9bx78 homo sapien
6	1022.5	60.3	286	2	Q71RB9	Q71rb9 homo sapien
7	832.5	49.1	670	2	O70491	O70491 mus musculu
8	832.5	49.1	670	2	Q6DIA8	Q6dia8 mus musculu
9	133	7.8	322	2	Q69ZH3	Q69zh3 mus musculu
10	133	7.8	621	2	Q8C7I6	Q8c7i6 mus musculu
11	133	7.8	621	2	Q9DBN1	Q9dbn1 m mus muscu
12	115.5	6.8	618	2	Q8PBV8	Q8pbv8 xanthomonas
13	100.5	5.9	572	2	Q7NYU4	Q7nyu4 chromobacte
14	100	5.9	2170	2	Q7TNJ2	Q7tnj2 rattus norv
15	98.5	5.8	1841	2	Q9ER60	Q9er60 mus musculu
16	98	5.8	525	2	Q6D2F7	Q6d2f7 erwinia car
17	97.5	5.8	403	1	GC5B_HUMAN	Q9nzh0 homo sapien
18	97.5	5.8	494	2	Q7MSH9	Q7msh9 wolinella s
19	97	5.7	336	2	Q7NRX1	Q7nrx1 chromobacte
20	97	5.7	595	2	Q6ZRS5	Q6zrs5 homo sapien
21	96.5	5.7	593	2	O83179	O83179 treponema p
22	96.5	5.7	1514	2	Q82BH0	Q82bh0 streptomyce
23	96	5.7	913	2	Q6CKC6	Q6ckc6 kluyveromyc
24	95.5	5.6	275	2	Q888F0	Q888f0 pseudomonas
25	95.5	5.6	526	2	Q8NP08	Q8np08 corynebacte
26	95	5.6	273	2	Q7WAG2	Q7wag2 bordetella
27	95	5.6	273	2	Q7WJK9	Q7wjk9 bordetella
28	94.5	5.6	378	2	Q71ES1	Q71es1 betta anaba
29	94.5	5.6	482	2	Q8M258	Q8m258 pfiesteria
30	94.5	5.6	540	2	Q69YS5	Q69ys5 homo sapien
31	94	5.5	465	2	Q72WP1	Q72wp1 desulfovibr
32	94	5.5	476	1	TRI6_HUMAN	Q15654 homo sapien
33	93.5	5.5	378	2	Q6VVU0	Q6vvu0 herichthys
34	93	5.5	279	2	Q8DM47	Q8dm47 synechococc
35	93	5.5	1962	2	Q75RX9	Q75rx9 homo sapien
36	93	5.5	2016	1	CIN5_HUMAN	Q14524 homo sapien
37	93	5.5	2016	2	Q75RY0	Q75ry0 homo sapien
38	92.5	5.5	378	2	Q71ES2	Q71es2 betta hippo
39	92	5.4	796	2	Q9P3B4	Q9p3b4 neurospora
40	92	5.4	2008	2	Q96S58	Q96s58 homo sapien
41	92	5.4	2146	2	Q8IZY2	Q8izy2 homo sapien
42	92	5.4	2146	2	Q9BZC4	Q9bzc4 homo sapien
43	92	5.4	2146	2	Q9NR73	Q9nr73 homo sapien
44	91.5	5.4	353	2	Q8M6Z9	Q8m6z9 pfiesteria
45	91.5	5.4	378	2	Q71ES3	Q71es3 betta pi. c

ALIGNMENTS

RESULT 1
Q7L9G1
ID Q7L9G1 PRELIMINARY; PRT; 560 AA.
AC Q7L9G1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein FLJ12541.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK022603; BAB14122.1; -.
SQ SEQUENCE 560 AA; 61987 MW; DF0FFED7687AED74 CRC64;

Query Match 65.5%; Score 1110.5; DB 2; Length 560;
Best Local Similarity 76.6%; Pred. No. 2.3e-81;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

Qy 1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD----------GQFSWNLFS 42

```
                |||||||||||||||||||||||||     |  | : |              | |  ||
Db        258 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 317

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        318 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 377

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
                |||||||||||||||||||||||||||||||||||||||||||||
Db        378 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 437

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                   :::  |      ||||||||||||||||||||||||||||||||||||||||||||||
Db        438 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 497

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
                |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        498 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 557

Qy        264 AQP 266
                |||
Db        558 AQP 560
```

RESULT 2
Q8TB21
ID Q8TB21 PRELIMINARY; PRT; 667 AA.
AC Q8TB21;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Stimulated by retinoic acid gene 6.
GN Name=FLJ12541;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC025256; AAH25256.1; -.
SQ SEQUENCE 667 AA; 73532 MW; 120685F4635CB0E5 CRC64;

Query Match 65.5%; Score 1110.5; DB 2; Length 667;
Best Local Similarity 76.6%; Pred. No. 2.8e-81;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

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Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
                |||||||||||||||||||||||||     |  | : |              | |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------- 149
                |||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                   :::  |      ||||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
                |||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
                |||
Db        665 AQP 667
```

RESULT 3
Q9BX79
ID Q9BX79 PRELIMINARY; PRT; 667 AA.
AC Q9BX79; Q9H9U8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE STRA6 isoform 1.
GN ORFNames=UNQ3126;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Szeto W., Jiang W., Tice D.A., Rubinfeld B., Hollingshead P.G.,
RA Fong S.E., Dugger D.L., Pham T., Yansura D.G., Wong T.A.,
RA Grimaldi J.C., Corpuz R.T., Singh J.S., Frantz G.D., Devaux B.,
RA Crowley C.W., Schwall R.H., Eberhard D.A., Rastelli L., Polakis P.,
RA Pennica D.;
RT "Overexpression of the retinoic acid-responsive gene Stra6 in human
RT cancers and its synergistic induction by Wnt-1 and retinoic acid.";
RL Cancer Res. 0:0-0(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AF352728; AAK30289.1; -.
DR EMBL; AY359089; AAQ89447.1; -.
SQ SEQUENCE 667 AA; 73502 MW; D20840A46998BA2E CRC64;

Query Match 65.5%; Score 1110.5; DB 2; Length 667;
Best Local Similarity 76.6%; Pred. No. 2.8e-81;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

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Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
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                ||||||||||||||||||||||||||      |  | : |                |  |  ||
Db        365 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 424

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                  |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        425 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 484

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------ 149
                  |||||||||||||||||||||||||||||||||||||||||||||
Db        485 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 544

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                  :::  |      ||||||||||||||||||||||||||||||||||||||||||||
Db        545 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 604

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
                  |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        605 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 664

Qy        264 AQP 266
                  |||
Db        665 AQP 667
```

RESULT 4
Q7Z3U9
ID Q7Z3U9 PRELIMINARY; PRT; 708 AA.
AC Q7Z3U9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein DKFZp686P1959 (Fragment).
GN Name=DKFZp686P1959;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Human endometrium;
RA Poustka A., Albert R., Moosmayer P., Schupp I., Wellenreuther R.,
RA Mewes H.W., Weil B., Amid C., Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BX537413; CAD97655.1; -.
KW Hypothetical protein.
FT NON_TER 1 1
SQ SEQUENCE 708 AA; 77825 MW; DB88B84AEAD286ED CRC64;

Query Match 65.5%; Score 1110.5; DB 2; Length 708;
Best Local Similarity 76.6%; Pred. No. 3e-81;
Matches 232; Conservative 4; Mismatches 30; Indels 37; Gaps 4;

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Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
                ||||||||||||||||||||||||     |  | : |              | |  ||
Db        406 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHQSPHPSRQAIFCWMSFS 465

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                  |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        466 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 525

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------ 149
                  |||||||||||||||||||||||||||||||||||||||||||||
Db        526 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMVATWRVLLSALYNAIHL 585

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                  :::  |      ||||||||||||||||||||||||||||||||||||||||||||
Db        586 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 645

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
                  |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        646 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 705

Qy        264 AQP 266
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                  |||
Db        706 AQP 708
```

RESULT 5
Q9BX78
ID Q9BX78 PRELIMINARY; PRT; 658 AA.
AC Q9BX78;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE STRA6 isoform 2.
GN ORFNames=UNQ3126;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Szeto W., Jiang W., Tice D.A., Rubinfeld B., Hollingshead P.G.,
RA Fong S.E., Dugger D.L., Pham T., Yansura D.G., Wong T.A.,
RA Grimaldi J.C., Corpuz R.T., Singh J.S., Frantz G.D., Devaux B.,
RA Crowley C.W., Schwall R.H., Eberhard D.A., Rastelli L., Polakis P.,
RA Pennica D.;
RT "Overexpression of the retinoic acid-responsive gene Stra6 in human
RT cancers and its synergistic induction by Wnt-1 and retinoic acid.";
RL Cancer Res. 0:0-0(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
RA Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
RA Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,
RA Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S.,
RA Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,
RA Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,
RA Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A.,
RA Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.H., Yansura D.,
RA Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,
RA Godowski P.;
RT "The secreted protein discovery initiative (SPDI), a large-scale
RT effort to identify novel human secreted and transmembrane proteins: a
RT bioinformatics assessment.";
RL Genome Res. 13:2265-2270(2003).
DR EMBL; AF352729; AAK30290.1; -.
DR EMBL; AY358748; AAQ89108.1; -.
SQ SEQUENCE 658 AA; 72582 MW; 5405281727F647DD CRC64;

Query Match 65.3%; Score 1106.5; DB 2; Length 658;
Best Local Similarity 76.2%; Pred. No. 5.7e-81;
Matches 231; Conservative 5; Mismatches 30; Indels 37; Gaps 4;

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Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
                ||||||||||||||||||||||||     |  | : |              | |  ||
Db        356 CYISALVLSCLLTFLVLMRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFS 415

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                  |||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        416 AYQTAFICLGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVI 475

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXC------------ 149
                  |||||||||||||||||||||||||||||||||||||||||||||:
Db        476 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAIVATWRVLLSALYNAIHL 535

Qy        150 -SPSIAIRHP-----TPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                  :::  |      ||||||||||||||||||||||||||||||||||||||||||||
Db        536 GQMDLSLLPPRAATLDPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 595

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANG 263
                  |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        596 SLRPGEEDEGMQLLQTKDSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANG 655

Qy        264 AQP 266
                  |||
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Db        656 AQP 658


RESULT 6
Q71RB9
ID   Q71RB9      PRELIMINARY;      PRT;   286 AA.
AC   Q71RB9;
DT   05-JUL-2004 (TrEMBLrel. 27, Created)
DT   05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Hypothetical protein PP14296.
GN   Name=PP14296;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wan D.F., Qin W.X., Zhou X.M., Zhang P.P., Jiang H.Q., Zu J.R.;
RL   Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF370419; AAQ15255.1; -.
KW   Hypothetical protein.
SQ   SEQUENCE   286 AA;  31877 MW;  24E6A620844A5EFB CRC64;

  Query Match           60.3%;  Score 1022.5;  DB 2;  Length 286;
  Best Local Similarity   74.8%;  Pred. No. 1.4e-74;
  Matches  214;  Conservative    5;  Mismatches   30;  Indels   37;  Gaps    4;

Qy         18 MRSLVTHR-----LGSGGSGD------------GQFSWNLFSVPLPLPPLAGLLVQQII 59
              ||||||||     |  | : |                | |  ||         ||||||||
Db          1 MRSLVTHRTNLRALHRGAALDLSPLHRSPHPSRQAIFCWMSFSAYQTAFICLGLLVQQII 60

Qy         60 FFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVILQNMAAHWVFLETHDGH 119
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||||
Db         61 FFLGTTALAFLVLMPVLHGRNLLLFRSLESSWPFWLTLALAVILQNMAAHWVFLETHDGH 120

Qy        120 PQLTNRRVLYAATFLLFPLNVLVGAMXXXC--------------SPSIAIRHP-----TP 160
              |||||||||||||||||||||||:                    :::  |      |
Db        121 PQLTNRRVLYAATFLLFPLNVLVGAIVATWRVLLSALYNAIHLGQMDLSLLPPRAATLDP 180

Qy        161 GYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQDSLRPGEEDEGMQLLQTK 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQDSLRPGEEDEGMQLLQTK 240

Qy        221 DSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLGANGAQP 266
              |||||||||||| |||||||||||||||||||||||||||||||||
Db        241 DSMAKGARPGASRGRARWGLAYTLLHNPTLQVFRKTALLGANGAQP 286


RESULT 7
O70491
ID   O70491      PRELIMINARY;      PRT;   670 AA.
AC   O70491;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE   Retinoic acid-responsive protein.
GN   Name=Stra6;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95377533; PubMed=7649373; DOI=10.1006/dbio.1995.1226;
RA   Bouillet P., Oulad-Abdelghani M., Vicaire S., Garnier J.M.,
RA   Schuhbaur B., Dolle P., Chambon P.;
RT   "Efficient cloning of cDNAs of retinoic acid-responsive genes in P19
RT   embryonal carcinoma cells and characterization of a novel mouse gene,
RT   Stra1 (mouse LERK-2/Eplg2).";
RL   Dev. Biol. 170:420-433(1995).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97346723; PubMed=9203140; DOI=10.1016/S0925-4773(97)00039-7;
RA   Bouillet P., Sapin V., Chazaud C., Messaddeq N., Decimo D., Dolle P.,
RA   Chambon P.;
RT   "Developmental expression pattern of Stra6, a retinoic acid-responsive
RT   gene encoding a new type of membrane protein.";
RL   Mech. Dev. 63:173-186(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Bouillet P.;
RL   Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF062476; AAC16016.1; -.
DR   MGD; MGI:107742; Stra6.
DR   GO; GO:0016021; C:integral to membrane; TAS.
SQ   SEQUENCE   670 AA;  73774 MW;  6ACE69F3EE16A4F7 CRC64;

  Query Match           49.1%;  Score 832.5;  DB 2;  Length 670;
  Best Local Similarity   57.7%;  Pred. No. 8.1e-59;
  Matches  176;  Conservative   28;  Mismatches   62;  Indels   39;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              ||||||||||  |||:|:||| |||     |  | : |                || |
Db        366 CYISALVLSCASTFLLLIRSLRTHRANLQALHRGAALDLDPPLQSIHPSRQAIVSWMSFC 425

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                  ||||||:|||||||:||||| :|:|||||||  |||||:||||||:|||||
Db        426 AYQTAFSCLGLLVQQVIFFLGTTSLAFLVFVPLLHGRNLLLLRSLESTWPFWLTVALAVI 485

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXCSPSIAIRHPT--- 159
              |||:||:|:|| || |:|:|||||:|  |||||||:|:||||:       |:  : |
Db        486 LQNIAANWIFLRTHHGYPELTNRRMLCVATFLLFPINMLVGAIMAVWRVLISSLYNTVHL 545

Qy        160 ----------------PGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                             |||:||:|||:|| ||||| : |||:||| | |  ||   ||||
Db        546 GQMDLSLLPQRAASLDPGYHTYQNFLRIEASQSHPGVIAFCALLLHAPSPQPRPPLAPQD 605

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLG--A 261
              |||| ||:|||||||||| |||||     : |||||||||||||:|| ||| ||    |
Db        606 SLRPAEEEEGMQLLQTKDLMAKGAGHKGSQSRARWGLAYTLLHNPSLQAFRKAALTSAKA 665

Qy        262 NGAQP 266
              || ||
Db        666 NGTQP 670


RESULT 8
Q6DIA8
ID   Q6DIA8      PRELIMINARY;      PRT;   670 AA.
AC   Q6DIA8;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Stra6 protein.
GN   Name=Stra6;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
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RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC075657; AAH75657.1; -.
DR   GO; GO:0016021; C:integral to membrane; TAS.
SQ   SEQUENCE   670 AA;  73715 MW;  96F963788EF91249 CRC64;

  Query Match             49.1%;  Score 832.5;  DB 2;  Length 670;
  Best Local Similarity   57.7%;  Pred. No. 8.1e-59;
  Matches  176;  Conservative   28;  Mismatches   62;  Indels   39;  Gaps    4;

Qy          1 CYISALVLSCLLTFLVLMRSLVTHR-----LGSGGSGD------------GQFSWNLFS 42
              ||||||||||  |||:|:||| |||     |  | : |                ||  |
Db        366 CYISALVLSCASTFLLLIRSLRTHRANLQALHRGAALDLDPPLQSIHPSRQAIVSWMSFC 425

Qy         43 VPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAVI 102
                  ||||||:|||||||:|||||  :|:|||||||  |||||:||||||:|||||
Db        426 AYQTAFSCLGLLVQQVIFFLGTTSLAFLVFVPLLHGRNLLLLRSLESTWPFWLTVALAVI 485

Qy        103 LQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVLVGAMXXXCSPSIAIRHPT--- 159
              |||:||:|:|| || |:|:|||||:|  |||||||:|:||||:       |:  : |
Db        486 LQNIAANWIFLRTHHGYPELTNRRMLCVATFLLFPINMLVGAIMAVWRVLISSLYNTVHL 545

Qy        160 ---------------PGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQD 203
                            |||:||:|||:|| ||||| : |||:||| | |  ||   ||||
Db        546 GQMDLSLLPQRAASLDPGYHTYQNFLRIEASQSHPGVIAFCALLLHAPSPQPRPPLAPQD 605

Qy        204 SLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYTLLHNPTLQVFRKTALLG--A 261
              |||| ||:|||||||||| |||||     : |||||||||||||:|| ||| ||    |
Db        606 SLRPAEEEEGMQLLQTKDLMAKGAGHKGSQSRARWGLAYTLLHNPSLQAFRKAALTSAKA 665

Qy        262 NGAQP 266
              || ||
Db        666 NGTQP 670


RESULT 9
Q69ZH3
ID   Q69ZH3      PRELIMINARY;      PRT;   322 AA.
AC   Q69ZH3;
DT   25-OCT-2004 (TrEMBLrel. 28, Created)
DT   25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   MKIAA1529 protein (Fragment).
GN   Name=mKIAA1529;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Embryonic intestinal tract;
RA   Okazaki N., Kikuno R.F., Ohara R., Inamoto S., Koseki H., Hiraoka S.,
RA   Saga Y., Seino S., Nishimura M., Kaisho T., Hoshino K., Kitamura H.,
RA   Nagase T., Ohara O., Koga H.;
RT   "Prediction of the Coding Sequences of Mouse Homologues of KIAA Gene:
RT   IV. The Complete Nucleotide Sequences of 500 Mouse KIAA-Homologous
RT   cDNAs Identified by Screening of Terminal Sequences of cDNA Clones
RT   Randomly Sampled from Size-Fractionated Libraries.";
RL   DNA Res. 11:205-218(2004).
DR   EMBL; AK173193; BAD32471.1; -.
FT   NON_TER       1      1
SQ   SEQUENCE   322 AA;  36477 MW;  AD7B68DFC7A34578 CRC64;

  Query Match              7.8%;  Score 133;  DB 2;  Length 322;
  Best Local Similarity   23.1%;  Pred. No. 0.012;
  Matches   55;  Conservative   37;  Mismatches   92;  Indels   54;  Gaps    7;

Qy         50 LAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAV---ILQNM 106
              | | |:  ::  |    | : :::|::| | |     |:      |||:: |   |||
Db         89 LWGYLIIHVVQSLCGVMLMYGLVLPIIHHRGL---EMLQGFGLGVLTLSIVVGLIILQVW 145

Qy        107 AAHWVFLETHDGHPQ------LTNRRVLYAATFLLFPLNVLVGAMXXXCSPSIAI----- 155
               |   ||:   |        | |||  :   : ||  |||:|     |   : |
Db        146 IAGTFFLQPKLGTSDKQKPLALNNRRAFHNFNYFLFFYNVLLG--LGACLSRLLISCLLG 203

Qy        156 ----------------RHPTPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMA 199
                             |:  :   | ::   ::| : :|| :|: :
Db        204 TWLIARIDRTIMQSGYEGADMGFGAWIGMLFVDHYHTNPVLVSFCHILITS--------- 254

Qy        200 APQDSLRPGEEDEGMQLLQTKDSMAKGARPG-AXRGRARWGLAYTLLHNPTLQVFRKT 256
                      :|  :|       : : | |  : | | || |  ||::|| | : ||:
Db        255 ---------HKDRKLQKTVKYWCLNQSAGPRFSARARTRWFLLQTLINNPRLVMLRKS 303


RESULT 10
Q8C7I6
ID   Q8C7I6      PRELIMINARY;      PRT;   621 AA.
AC   Q8C7I6;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched
DE   library, clone:C730023F16 product:hypothetical protein, full insert
DE   sequence.
GN   Name=1300002K09Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
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RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK050152; BAC34096.1; -.
DR   MGD; MGI:1921402; 1300002K09Rik.
KW   Hypothetical protein.
SQ   SEQUENCE   621 AA;  70903 MW;  7FAAC08C5CD00BBA CRC64;

  Query Match             7.8%;  Score 133;  DB 2;  Length 621;
  Best Local Similarity   23.1%;  Pred. No. 0.025;
  Matches   55;  Conservative   37;  Mismatches   92;  Indels   54;  Gaps    7;

Qy         50 LAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAV---ILQNM 106
              | | |:  ::  |    | : :::|::| | |     |:      |||:: |   |||
Db        388 LWGYLIIHVVQSLCGVMLMYGLVLPIIHHRGL---EMLQGFGLGVLTLSIVVGLIILQVW 444

Qy        107 AAHWVFLETHDGHPQ------LTNRRVLYAATFLLFPLNVLVGAMXXXCSPSIAI----- 155
               |   ||:   |         | |||  :   : ||  |||:|     |   : |
Db        445 IAGTFFLQPKLGTSDKQKPLALNNRRAFHNFNYFLFFYNVLLG--LGACLSRLLISCLLG 502

Qy        156 ----------------RHPTPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMA 199
                            |:  :   | ::   ::| : :|| :|: :
Db        503 TWLIARIDRTIMQSGYEGADMGFGAWIGMLFVDHYHTNPVLVSFCHILITS--------- 553

Qy        200 APQDSLRPGEEDEGMQLLQTKDSMAKGARPG-AXRGRARWGLAYTLLHNPTLQVFRKT 256
                  :|  :|       : : | |  : | | || |  ||::|| | : ||:
Db        554 ---------HKDRKLQKTVKYWCLNQSAGPRFSARARTRWFLLQTLINNPRLVMLRKS 602


RESULT 11
Q9DBN1
ID   Q9DBN1      PRELIMINARY;      PRT;   621 AA.
AC   Q9DBN1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE   Mus musculus adult male liver cDNA, RIKEN full-length enriched
DE   library, clone:1300002K09 product:hypothetical protein, full insert
DE   sequence (Mus musculus adult male liver tumor cDNA, RIKEN full-length
DE   enriched library, clone:C730040D15 product:hypothetical protein, full
DE   insert sequence).
GN   Name=1300002K09Rik;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RX   MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA   Carninci P., Hayashizaki Y.;
RT   "High-efficiency full-length cDNA cloning.";
RL   Meth. Enzymol. 303:19-44(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RX   MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA   RIKEN FANTOM Consortium;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RX   MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA   Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA   Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT   "Normalization and subtraction of cap-trapper-selected cDNAs to
RT   prepare full-length cDNA libraries for rapid discovery of new genes.";
RL   Genome Res. 10:1617-1630(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RX   MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA   Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA   Konno H., Akiyama J., Nishi K., Kitsunai T., Tashiro H., Itoh M.,
RA   Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA   Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA   Fujiwake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA   Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA   Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT   "RIKEN integrated sequence analysis (RISA) system-384-format
RT   sequencing pipeline with 384 multicapillary sequencer.";
RL   Genome Res. 10:1757-1771(2000).
RN   [6]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RA   Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,
RA   Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA   Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,
RA   Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA   Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
RA   Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
RA   Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,
RA   Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA   Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA   Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA   Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN   [7]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Liver;
RA   Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA   Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA   Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA   Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA   Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA   Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA   Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA   Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA   Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA   Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA   Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK004855; BAB23619.1; -.
DR   EMBL; AK050348; BAC34204.1; -.
DR   MGD; MGI:1921402; 1300002K09Rik.
KW   Hypothetical protein.
```

```
SQ   SEQUENCE   621 AA;  71002 MW;  909E1C6BC2A9EA60 CRC64;

  Query Match             7.8%;  Score 133;  DB 2;  Length 621;
  Best Local Similarity   23.1%;  Pred. No. 0.025;
  Matches   55;  Conservative   37;  Mismatches   92;  Indels   54;  Gaps    7;

Qy         50 LAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFWLTLALAV---ILQNM 106
              | | |:  ::  |    | : :::|::| | |     |:     |||:: |   |||
Db        388 LWGYLIIHVVQSLCGVMLMYGLVLPIIHHRGL---EMLQGFGLGVLTLSIVVGLIILQVW 444

Qy        107 AAHWVFLETHDGHPQ------LTNRRVLYAATFLLFPLNVLVGAMXXXCSPSIAI----- 155
               |   ||:   |        | |||  :   : ||  |||:|     |   : |
Db        445 IAGTFFLQPKLGTSDKQKPLALNNRRAFHNFNYFLFFYNVLLG--LGACLSRLLISCLLG 502

Qy        156 ---------------RHPTPGYYTYRNFLKIEVSQSHPAMTAFCSLLLQAQSLLPRTMA 199
                            |:  :   | ::   ::| : :|| :|: :
Db        503 TWLIARIDRTIMQSGYEGADMGFGAWIGMLFVDHYHTNPVLVSFCHILITS--------- 553

Qy        200 APQDSLRPGEEDEGMQLLQTKDSMAKGARPG-AXRGRARWGLAYTLLHNPTLQVFRKT 256
                    :|  :|      : : | |  : | | || |  ||::|| | : ||:
Db        554 ---------HKDRKLQKTVKYWCLNQSAGPRFSARARTRWFLLQTLINNPRLVMLRKS 602


RESULT 12
Q8PBV8
ID   Q8PBV8      PRELIMINARY;      PRT;   618 AA.
AC   Q8PBV8;
DT   01-OCT-2002 (TrEMBLrel. 22, Created)
DT   01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   Hypothetical protein XCC1009.
GN   OrderedLocusNames=XCC1009;
OS   Xanthomonas campestris (pv. campestris).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC   Xanthomonadaceae; Xanthomonas.
OX   NCBI_TaxID=340;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 33913 / NCPPB 528;
RX   MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA   da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA   Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA   Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA   Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA   Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA   Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA   Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA   Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA   Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA   Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA   Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA   Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA   Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA   Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA   Setubal J.C., Kitajima J.P.;
RT   "Comparison of the genomes of two Xanthomonas pathogens with differing
RT   host specificities.";
RL   Nature 417:459-463(2002).
DR   EMBL; AE012197; AAM40309.1; -.
KW   Complete proteome.
SQ   SEQUENCE   618 AA;  67854 MW;  93B6E2A062AD6B69 CRC64;

  Query Match             6.8%;  Score 115.5;  DB 2;  Length 618;
  Best Local Similarity   23.0%;  Pred. No. 0.66;
  Matches   90;  Conservative   40;  Mismatches   97;  Indels  165;  Gaps   22;

Qy          3 ISALVLSCLLTFLVLMRSLVTHRLGSGGSGDGQPSWNLFSVPLPLPPLAGLLVQQIIFFL 62
              | | ::: || : ::  ||   | |||||   :  |  |          |||
Db        246 IQAALVTPLLAWAMVKVSLAGTRAGSGGS---RAQWRYF----------GLLG-------- 285

Qy         63 GTTALAFLVLMPVLHGRNLLFFRSLES---SWPFWLTLALAVILQNMAAHWVFLETHDGH 119
              | : ||  ||          ||   |     ||    ||| |    :   |
Db        286 GISTLAIFVLG---------FFSDAERISFHWPLPGYLALLVAAPVILMRW--------- 327

Qy        120 PQLTNRRVLYAATFLLFPLNVLVGAMXXXCSPSI-AIRHPTPG--YYTYRNF-------- 168
                 | |  ||:|:  | :| ||      : |: |||     |  ||  |||
Db        328 -----PRPLRRATWLIALLGML-GAYSYYLAVSVPAIRAQAAGEKYYP-RNFAGWKDLAR 380

Qy        169 -LKIEVSQSHPAMTAFCSLLLQAQSLLPRTMAAPQDSLRPGEE------DEGMQLLQT-- 219
               :| |::|  |                  | :|   :: : | |      |  :::||
Db        381 AVKTELAQLPPG--------------TRVLA---ENFKVGAELGFQLHDAQIEVLQADL 422

Qy        220 KDSMAKGARPGAXRGRARWGL--------AYTLLHNPTLQVFRK--------TALLGA-- 261
               |   : |:       |:|||           |: :|: | :|          |::|
Db        423 NDKHGRSAQ------LAQWGLLSHGERSGPRLLVLSPSDQRYRDLLTRYHAICAMVGPLP 476

Qy        262 --------NGAQ-------PCSSLPGSPPSITPAM------------------------ 281
                     :| |       |    || | | |||
Db        477 PPKVVSTDHGYQRFLLFALPAQRQPG--PCIAPAMAWIDTPLPGVAATTTMQVRGWAFKD 534

Qy        282 ------------QPAGPPDHXGXVEVCLHWE 300
                         :|||  |:   ::|  :|:
Db        535 GVGLSRVELLVDGRPAGRADYGATLDVRPYWK 566


RESULT 13
Q7NYU4
ID   Q7NYU4      PRELIMINARY;      PRT;   572 AA.
AC   Q7NYU4;
DT   01-MAR-2004 (TrEMBLrel. 26, Created)
DT   01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Probable periplasmic binding protein.
GN   OrderedLocusNames=CV1178;
OS   Chromobacterium violaceum.
OC   Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC   Neisseriaceae; Chromobacterium.
OX   NCBI_TaxID=536;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 12472 / DSM 30191;
RX   MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA   Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA   Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA   Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA   Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA   Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA   Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA   Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA   Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA   Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA   Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA   Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA   Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA   Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA   Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA   Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA   di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA   Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA   Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA   Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA   Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA   Santos E.B.P., Santos F.R., Schneider M.P.C., Seuanez H.N.,
RA   Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA   Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA   Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA   Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
RT   "The complete genome sequence of Chromobacterium violaceum reveals
RT   remarkable and exploitable bacterial adaptability.";
RL   Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
CC   -!- SIMILARITY: Belongs to the bacterial extracellular solute-binding
CC       protein family 5.
DR   EMBL; AE016914; AAQ58853.1; -.
DR   GO; GO:0005215; F:transporter activity; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR002345; Lipocalin.
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DR   InterPro; IPR000914; SBP_bac_5.
DR   InterPro; IPR009058; Wing_hlx_DNA_bnd.
DR   Pfam; PF00496; SBP_bac_5; 1.
DR   PROSITE; PS00213; LIPOCALIN; UNKNOWN_1.
KW   Complete proteome.
SQ   SEQUENCE   572 AA;  65364 MW;  937A150164700A29 CRC64;

  Query Match             5.9%;  Score 100.5;  DB 2;  Length 572;
  Best Local Similarity   23.7%;  Pred. No. 9.8;
  Matches   64;  Conservative   26;  Mismatches   79;  Indels  101;  Gaps   14;

Qy         17 LMRSLVTHRLGSGGSGDGQFSWNLFSVPLPLPPLA----------GLLVQQIIFFLGTT 65
              |: ||  | ||:| ||         :|:|  ||             ||:||  |
Db        122 LLASLPQH-LGAGDSG------RSLRIPIPHAPLTLDPQRVNARLESHLVRQIFDRLCRH 174

Qy         66 ALAFLVLMPVL--------HGRNLLFFRSLESSWPFWLTLALAVILQNMAAHWVFLETHD 117
                 || | |         |||          | |||                  |  ||
Db        175 DRLGQVLRPALAHHWEADPEGRN----------WRFWLRPG-------------LRFHD 210

Qy        118 GHPQLTNRRVLYAATFLLFPLNVLVGAMXXXCSPSIAIRHPTPGYYT-YRNFLKIEVSQS 176
              | |       | | |              :  : :: |   |:  | :  :::|
Db        211 GGP-------LDAET--------------AAASLLRLKQPDNPYHALYAHLRRVDV--- 245

Qy        177 HPAMTAFCSLLLQAQSLLPRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRA 236
              | |::  |  | :|  | |: :|    |: |      |:  |  : |  |: |
Db        246 HDALSFSCR-LTEADHLWPQRLATANASIVP------MRRSQDFERMPVGSGPFRVE--- 295

Qy        237 RWGLAYTLLHNPTL-------QVFRKTALL 259
                 ||:|       | :|: |||
Db        296 --------LHSPQRLKLAAFEQHYRERALL 317


RESULT 14
Q7TNJ2
ID   Q7TNJ2      PRELIMINARY;      PRT;  2170 AA.
AC   Q7TNJ2;
DT   01-OCT-2003 (TrEMBLrel. 25, Created)
DT   01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   ATP-binding cassette transporter sub-family A member 7.
GN   Name=ABCA7;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Wister; TISSUE=Platelet;
RA   Sasaki M., Nada S., Yamaguchi A.;
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: Belongs to the ABC transporter family.
DR   EMBL; AB097814; BAC81426.1; -.
DR   HSSP; P58301; 1F2T.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0006810; P:transport; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR003439; ABC_transporter.
DR   Pfam; PF00005; ABC_tran; 2.
DR   ProDom; PD000006; ABC_transporter; 2.
DR   SMART; SM00382; AAA; 2.
DR   PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR   PROSITE; PS50893; ABC_TRANSPORTER_2; 2.
KW   ATP-binding.
SQ   SEQUENCE   2170 AA;  237718 MW;  003C8DF70B8744CE CRC64;

  Query Match             5.9%;  Score 100;  DB 2;  Length 2170;
  Best Local Similarity   23.7%;  Pred. No. 46;
  Matches   82;  Conservative   62;  Mismatches  124;  Indels   78;  Gaps   19;

Qy          3 ISALVLSCL---LTF------LVLMRSLVTH----RLGSGGSGD----GQFSWNLFSVPL 45
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              :  ||  |:   ::|      |||:   :|     :| ||        | | |:: :
Db       1559 VDVLVSICVVFAMSFVPASFTLVLIEERITRAKHLQLVSGLPQTLYWLGNFLWDMCNY-- 1616

Qy         46 PLPPLAGLLVQQIIF-------FLGTTALAFLVLMPVLHGRNLL-------FFRSLESSW 91
                 |  : :  :||       ::    |  |:|: :|:| ::        || |: |:
Db       1617 ----LVAVCIVVLIFLAFQQKAYVAPENLPALLLLLLLYGWSITPLMYPASFFFSVPSTA 1672

Qy         92 PFWLT-LALAVILQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPLNVL-VGAMXXXC 149
              || : | : : :  | :|     | : |  :|  :    ||:||   |  | :
Db       1673 YVVLTCINLFIGINSSMATFVLELLSDQNLQEVSR--ILKQVFLIFPHFCLGRGLIDMVR 1730

Qy        150 SPSIAIRHPTPGYYTYRNFLKIE-VSQSHPAMTA------FCSLLLQAQS-LLPRTMAAP 201
              : ::|       |   ::: |: : : ::  || |        :|||| :: |||:    |
Db       1731 NQAMADAFERLGDKQFQSPLRWDIIGKNLLAMVAQGPLFLLITLLLQHRNRLLPQ----P 1786

Qy        202 QDSLRP--GEEDEGMQLLQTKDSMAKGARPG----------AXRGRARWGLAYTLLHNPT 249
              :  | |  |||||   ::: :: : |||  |           ||:    : :  |  |
Db       1787 KSRLPPPLGEEDE--DVVRERERVTKGATQGDVLVLRDLTKVYRGQRSPAVDHLCLGIPP 1844

Qy        250 LQVFRKTALLGANGAQPCS--------SLPGSPPSITPAMQPAGPP 287
              : |     ||| |||   |         :|| |  ::      | |
Db       1845 GECF---GLLGVNGAGKTSTFRMVTGDTLPSSGEAVLAGHNVAQEP 1887


RESULT 15
Q9ER60
ID   Q9ER60      PRELIMINARY;      PRT;  1841 AA.
AC   Q9ER60;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE   Voltage-gated sodium channel.
GN   Name=Scn4a;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=balb/c; TISSUE=Heart;
RX   MEDLINE=21823196; PubMed=11834499;
RA   Zimmer T., Benndorf K.;
RT   "The mouse heart sodium channel (mH1): cloning and characterization of
RT   alternatively spliced variants.";
RL   Am. J. Physiol. Heart Circ. Physiol. 282:H1007-H1017(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- SIMILARITY: Belongs to the sodium channel family.
DR   EMBL; AJ278787; CAC17146.1; -.
DR   HSSP; P04775; 1BYY.
DR   MGD; MGI:98250; Scn4a.
DR   GO; GO:0016021; C:integral to membrane; TAS.
DR   InterPro; IPR001682; Ca/Na_pore.
DR   InterPro; IPR002111; Cat_channel_TrpL.
DR   InterPro; IPR005821; Ion_trans.
DR   InterPro; IPR000048; IQ_region.
DR   InterPro; IPR005820; M+channel_nlg.
DR   InterPro; IPR001696; Na_channel.
DR   InterPro; IPR008052; Na_channel4.
DR   InterPro; IPR010526; Na_trans_assoc.
DR   Pfam; PF00520; Ion_trans; 4.
DR   Pfam; PF00612; IQ; 1.
DR   Pfam; PF06512; Na_trans_assoc; 1.
DR   PRINTS; PR00170; NACHANNEL.
DR   PRINTS; PR01665; NACHANNEL4.
DR   SMART; SM00015; IQ; 1.
DR   PROSITE; PS50096; IQ; 1.
KW   Ion transport; Ionic channel; Sodium channel; Sodium transport;
KW   Transmembrane; Transport; Voltage-gated channel.
SQ   SEQUENCE   1841 AA;  208796 MW;  0766DFD33A9E0E55 CRC64;

  Query Match             5.8%;  Score 98.5;  DB 2;  Length 1841;
  Best Local Similarity   22.0%;  Pred. No. 51;
  Matches   67;  Conservative   35;  Mismatches  105;  Indels   97;  Gaps   14;
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Qy         35 QFSWNLFSVPLPLPPLAGLLVQQIIFFLGTTALAFLVLMPVLHGRNLLFFRSLESSWPFW 94
              |  ||:|           :|   :  ||   || :  : ||    ||     |  |||
Db        633 QQGWNIFD---------SFIVTLSLVELG---LANVQGLSVLRSFRLLRVFKLAKSWP-T 679

Qy         95 LTLALAVILQNMAAHWVFLETHDGHPQLTNRRVLYAATFLLFPL--NVLVGAMXXXCSPS 152
              | : : :|  :: |              | |  :: |    :| :    | |     |
Db        680 LNMLIKIIGNSVGA------------LGNLTLVLAIIVFIFAVVGMQLFGKSYKECVCK 726

Qy        153 IAIRHPTPGYYT---YRNFLKI---------------EVSQSHPAMTAFCSLLLQAQ-- 191
              ||     | ::    : :|| :                ||:     :| |  :::
Db        727 IASDCSLPRWHMHDFFHSFLIVFRILCGEWIETMWDCMEVAGQAMCLTVFLMVMVIGNLV 786

Qy        192 ------SLLPRTMAAPQDSLRPGEEDEGMQLLQTKDSMAKGARPGAXRGRARWGLAYT-- 243
                  :||  : :|  |||   :||  |  ||               || :||:|:
Db        787 VLNLFLALLLSSFSA--DSLAASDEDGEMNNLQ-----------IAIGRIKWGIAFAKT 832

Qy        244 ----LLHNPTLQVFRKTALL--------GANGAQPCSSLPGSPPSITPAMQPAGPPDHXG 291
                 |||   | :  |  :|        | ||  |            |  :   ||   |
Db        833 FLLGLLHGKILSL--KDIMLSLGEPGGAGENGESP-----------PEDEKKEPPPEDG 878

Qy        292 XVEV 295
                |:
Db        879 NKEL 882
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Search completed: February 8, 2005, 13:40:10
Job time : 145.653 secs